#### STIC-Biotech/ChemLib

34254

From: Sent:

Chan, Christina

T: Subject: Tuesday, January 14, 2003 3:04 PM Yu, Misook; STIC-Biotech/ChemLib RE: rush search for 09/648,310

Importance:

High

#### Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From: Yu, Misook

Sent: Tuesday, January 14, 2003 11:43 AM

To: Chan, Christina

Subject:

rush search for 09/648,310

Please approve rush searh. The case is due this bi-week.

Please search SEQ ID NO:1 and 2.

Examiner Misock YUNPh D 703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

Chi

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: 36B	TYPE OF SEARCH: NA Sequences:	VENDOR/COST (where applic.) STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up:	Bibliographic:	DRLink:
Date Completed: 1-17-03	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

## BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the BioTech-Chem searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Volu	ntary Results Feedback Form
>	I am an examiner in Workgroup: (Example: 1610)
>	Relevant prior art found, search results used as follows:
	102 rejection
	103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
•	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Search results were not useful in determining patentability or understanding the invention.
Othe	r Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

#### Yu, Misook

To:

Chan, Christina

Subject:

rush search for 09/648,310

Please approve rush searh. The case is due this bi-week.

Please search SEQ ID NO:1 and 2.

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

OM nucleic - nucleic search, using sw model

January 16, 2003, 21:46:28; Search time 102 Seconds Run on:

(without alignments) 3409.581 Million cell updates/sec

US-09-648-310-1

1 ggcacgagctctcctcgtcc.....gtaataaaaaaaaatcatgt 780 Perfect score: Sequence:

Scoring table:

393868 seqs, 222934149 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_NA:\* .: /cgn2\_6/ptodata/2/pubpna/US07\_

/ptodata///pubpna/PCT\_NEW\_PUB.seq:\*/ /ptodata///pubpna/USOG\_NEW\_PUB.seq:\*/ /ptodata///pubpna/USOG\_NEW\_PUB.seq:\*/ /ptodata///pubpna/USOT\_NEW\_PUB.seq:\*/ /ptodata//pubpna/USOT\_NEW\_PUB.seq:\*/

cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*/cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*/cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:/cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:/cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:/cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:/cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*/cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seg:

Description	Sequence 545, App Sequence 939, App Sequence 939, App Sequence 318, App Sequence 2101, Ap Sequence 2101, Ap Sequence 2101, Ap Sequence 2020, Ap Sequence 105, App Sequence 105, App Sequence 30, Appl Sequence 3415, App Sequence 342, App Sequence 342, App Sequence 342, App Sequence 355, Ap Sequence 355, App Sequence 355, App Sequence 356, App Sequence 356, App Sequence 356, App Sequence 356, App
SUMMARIES	US-09-925-300-545 US-09-920-300-939 US-09-925-299-318 US-09-938-842A-355 US-09-938-842A-355 US-09-880-107-687 US-09-880-107-687 US-09-284-0938-4150 US-09-294-0938-4150 US-09-338-841.55 US-09-338-842A-3235 US-09-938-842A-3570 US-09-938-842A-3570 US-09-938-842A-3570 US-09-938-842A-3570 US-09-938-842A-3570 US-09-925-301-565 US-09-925-301-565 US-09-925-301-565 US-09-925-820A-395
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10 US-09-813-742-1	10 US-09-790-988-1	Q IIC-00-038-8438-4733	75/4-W740 056 60 CO	10 US-09-969-373-912	10 US-09-969-373-913	9 IIS-09-754-8538-157	9 HS-09-754-8538-159	0 11C-00-030-040x-3300	0 110-00-754 0525	2-45-9-1-60 CO	9 US-U9-754-853A-3	10 US-09-739-457-5	10 US-09-969-373-1157	9 US-10-015-219-605	10 HS-00-777-564-60E	200-400-777-204-003	10 US-09-864-761-20733	10 US-09-864-761-3972	9 US-10-114-893-77	9 115-10-114-893-314	0 115-00-030-043%-4364	10 20 03 03 - 330 - 04 ZA - 4 Z04	10 US-09-960-352-15014	9 US-09-754-853A-4	10 US-09-962-832-117	10 US-09-867-701-131	10 US-09-790-988-1	10 US-09-878-574-4572	9 US-09-938-842A-3707
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## ALIGNMENTS

25; 1 36.9%; Score 288.2; DB 10; Length 778; Similarity 69.9%; Pred. No. 5.4e-68; Conservative 2; Mismatches 167; Indels 25; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101 CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 545
LENGTH: 778 NAME/KEY: misc feature LOCATION: (641) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (652)
COTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-545 Sequence 545, Application US/09925300 Patent No. US20020151681A1 APPLICANT: Craig Rosen, APPLICANT: Steve Ruben ORGANISM: Homo sapiens GENERAL INFORMATION: US-09-925-300-545 451; Query Match Best Local S Matches 451 TYPE: DNA FEATURE a οy ò qq

Gaps

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LENGTH:
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136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT 195
                                                                                                       272 ATTIGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAAC
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APPLICANT: King, Gordon E.
APPLICANT: Maedleine Joy
APPLICANT: Waedleine Joy
APPLICANT: Waedleine Joy
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT PILICA DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 4e-46;
0; Mismatches 144; Indels 23;
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68.7%;
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56; Conservative
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Best Local Simi
Matches 366;
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LENGTH: 552
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                                                  484
                                                                                                                                                                                                                                                                                                        193 TCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCAAGGATGGGAATG 134
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GATGATGTTGACATTATATACTGCAAGATTAATGTGGGTTTACATATCTTTATGTACTGC
                                                                                                                                                                                                                                                        133 TTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAG
                                                  ---TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCC
                                                                                                                                                                                603 ITAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAAGCTTT
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                                                                          TTATGTATTTTTATAGACCTTTGTAAACAAAGGGGA--CTTGTTGAGAAGTCCTGTTTT
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| Patent No. US20020131971a1
| GENERAL Information
| Fatent No. US20020131971a1
| GENERAL Information
| APPLICANT: King, Gordon E.
| APPLICANT: Meagher, Madeleine Joy
| APPLICANT: Xu, Jangchun
| APPLICANT: Scrist, Heather
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| FILE REFERENCE: 210121.547C1
| CURRENT APPLICATION NUMBER: US/10/033,528
| CURRENT FILING DATE: 2001-12-26
| NUMBER OF SEQ ID NOS: 1896
| SOFTWARRE: FastSEQ for Windows Version 4.0
| SEQ ID NO 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAA 773
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Pred. No. 4e-46;
0; Mismatches 144;
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Best Local Similarity 68.7%;
Matches 366; Conservative
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CORGANISM: Homo sapiens
US-10-033-528-939
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                                                                  603 TTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTT 662
                                                                                                                                    663 TGTTTTCTTAAACCATTCTTAGTCT--CTGCCACACTTGACACTCCGTCAAAGTGAGAAG 720
721 CGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAAA 773
                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 318
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature LOCATION: (150)
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (143)
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NAME/KEY: misc_feature
LOCATION: (144)
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LOCATION: (146)
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                                                                                                                                                                                                                                                                                                                             Sequence 318, Application US/09925299
Patent No. US20020055627Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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LOCATION: (159)
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LOCATION: (163)
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                                                                                                                                                                                                                                                                                               RESULT 4
US-09-925-299-318
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OTHER INFC
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169 AATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGAAATTCATCGTCTGGGTTCCAA 228
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65.8%; Pred. No. 1.4e-23;
live 0; Mismatches 81
                                                                                                                     O
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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S. OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-318
                                                                                                                                                                                                                                                                                                                            LOCATION: (223)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (242)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
                                                                                                                     or
                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature LOCATION: (198)
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                                                                                                                                                                                                                                                                                                                                                                                                            or
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LOCATION: (234)
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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INFORMATION: n equals a,t,g, or
                                                       OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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                                                                                                               OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                       INFORMATION: n equals
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Best Local Similarity 65.8
Matches 156; Conservative
                     NAME/KEY: misc_feature
                                                                                                                                                                                         NAME/KEY: misc_feature
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LOCATION: (227)
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LOCATION: (314)
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GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
                                                                                                                                                                                                                                                                                                                                                    TITIATAGACCITIGIAAACAAAAGGGGACT--IGTIGAGAAGTCCTGTTTTATACCTT 550
                                                                                                                                                                                                                                                                                                                                                                             671, TAAACCATTCTTAGTCT -- CTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAA 728
                                                                                                                                                                                                                                                                                    GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 TAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                               611 GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCT
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                                                                                                                                                                Length 365;
                                                                                                                                                                                                            Indels
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Fatent No. US2002017552A1
GENERAL INFORMATION:
APPLICANT: Jang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Barlocker, Susan L.
APPLICANT: Gerist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE T
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FEASEG for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACCAACTCCTATGAGAAATATTATGATGTTATGTAATAAAGA
                                                                                                                                                        Score 92.8; DB 9; 1
Pred. No. 1.3e-15;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%; Score 92.8; DB 9;
llarity 62.0%; Pred. No. 1.3e-15;
Conservative 0; Mismatches 123;
                                                                ; LOCATION: 273
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(365)
; OTHER INFORMATION: n - A,T,C or G
US-09-878-178-2101
                                                                                                                                                             11.9%;
62.0%;
                                                                                                                                                        Query Match 11.99
Best Local Similarity 62.09
Matches 214; Conservative
ORGANISM: Homo sapiens
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                                         NAME/KEY: misc_feature
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                                                                                                                                                                                           APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
SPRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGAACGTAGACGAAGAGATTCAGAAACTGGAAGAAGAGATCCATCGTCTTGGTTCTCG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
              229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC
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Patent No. US20020156011a1
GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Scotist, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACGCAGGAGACTGCTTTTGCAAGGTGTTCATGATGATGTTGACAT 396
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Pred. No. 4.5e-20;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 210121.527C1
CURRENT PELLING NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 365
                                                                                                                                                      Sequence 355, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-09-938-842A-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.1%;
Best Local Similarity 67.5%;
Matches 154; Conservative
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; Sequence 4150, Application US/09294093B

; Patent No. US20010051335Al

; GENERAL INFORMATION:

APPLICANT:

Lalgudi, Raghunath, V.
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ORGANISM: Zea mays
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US-09-294-093B-4150
                          US-09-294-093B-2020
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SEQ ID NO 4150
LENGTH: 289
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GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCT 670
                                                                                                                                           671 TAAACCATICTIAGICT--CIGCCACACTIGACACICCGICAAAGIGAGAGGGAACIAA 728
                                 233 TCTTGAAAGAAAATCTATGTATGATGCTATAAAATAAATCCTATTATTTTTCTCAGGAAT 174
                                                                                            436 GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 ITITATAGACCTITGTAAACAAAAGGGGACT--TGTTGAGAAGTCCTGTTTTATACCTT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 TCTTGAAAGAAAATCTATGATGATGATGATAAAAAAAATCCTATTATTTTCTCAGGAAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 TAAACCATTCTTAGTCT--CTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAA 728
                                                                                                                                                                            113 TARATRATTAGACATTITCTATAGATATTIGACATTCTGCGAAAGCAACAAGCAAACTGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 TANATANTTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA287347
US-09-880-107-687
                                                                                                                                                                                                                                                                                                                                       Sequence 687, 087,001

Sequence 687,00142981A1

Sequence 687,00142981A1

Setent No. US20020142981A1

SEPERAL INFORMATION:

APPLICANT: Workley, Joseph G.

APPLICANT: Gener, Due

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TURENT APPLICATION NUMBER: US/09/80,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

TEMPLY APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 406;
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                                                                                                                                                                                                                729 AGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAA 773
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.0
Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-880-107-687/c
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Sequence 2020, Application US/09294093B

Patent No. US20010051335A1

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION:
POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT FILING DATE: 1999-04-16
PRIOR PILING DATE: 1999-04-16
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SEQ ID NO 2020
LENGTH: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Lalgudi, X.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REPERENCE: PL-0009 US US/09/294,093B
CURRENT APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION BATE: 12, 1998
NUMBER OF SEQ ID NOS: 6207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 GCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 CAGCAGCCCGATGGCTCTTACAAGGTCAAGTTTGGCGTTCTCTTCAACGACGATCGGTGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700345395H1
US-09-294-093B-2020
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700353201H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.2%; Score 87.4; DB 10; Best Local Similarity 65.8%; Pred. No. 3.1e-14; Matches 127; Conservative 0; Mismatches 66;
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LOCATION: 9, 111, 148, 231, 265, 286
OTHER INFORMATION: a, t, c, g, or other
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Yun
APPLICANT: The Mang, Yun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFERENCE: SCRIP1300-3
CORRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4123 TTATTTTTAAAACCGTCCAATACCTTTTGTATTATGTAACATTCAAAAGACAATGTACTG 4182
                          4003 GTAAATACTATTTAATGAACGACTGTACAAAGTAGAATTCCTAGATGTATTTTTGTATG 4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 GTAAACTGGAATAATTAAGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTATAGAC 502
517 GGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAAT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACAT
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                                                                                                                                                                                                     Sequence 30, Application US/08927939
Patent No. US20010006640A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
FITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT APPLICATION NUMBER: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
SEC ID NO 30
                                                                                                                                                                                                                                                                                                                    methods to inhibit or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 38.4; DB 8;
llarity 48.6%; Pred. No. 1.8;
Conservative 0; Mismatches 111;
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                                                                                                3631 ATACAAAACCAGTTATTGCTT 3611
                                                                          577 AAACAAAACCTGTTATTTTT
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CDS (2669)...(2795)
CDS (2069)...(2795)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
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US-09-938-842A-3235
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US-08-927-939-30
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LOCATION:
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NAME/KEY:
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Best Local
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                                                                                                                                                                        AAAAATGCCGATGGGAAACTGGAGTGTGGGGTCCTCTTCCAAGACGACAGATGT.286
                                                                                                                                                                                                                                                     136 CAGCAGCCCGAINGCICITACAAGGICAAGIIIGGCGIICCICTICAACGACGAICGGIGI 195
                                                                                                                                                                                                                                                                               167 GCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCC 226
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                  Length 289;
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TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                       Indels
              8.1%; Score 63.2; DB 10;
ilarity 59.3%; Pred. No. 1e-07;
Conservative 0; Mismatches 82;
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Pred. No. 1.9;
0; Mismatches 64;
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CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
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PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105, Application US/10098841
Publication No. US20020197679A1
                                                                                                                                                                                                                                                                                                                                                          ACGAAGGCGANTGTTCTGCAAGTG 278
                                                                                                                                                                                                                                                                                                                                   347 ACGTACGCAGGAGAGCTGCTTTTG 370
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Best Local Similarity 54.6%;
Matches 77; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian, Xiaohong B.
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
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Chen, Rui-hong
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Zhao, Qing A.
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Wehrman, Tom
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; LOCATION: (707)..(3379)
US-10-098-841-105
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                                   Similarity
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US-10-098-841-105/c
                                   Best Local Sim
Matches 121;
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                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                          508 TAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTATACCTTGGAGCAAAACATTACAA 567
                                                                                                                                                                                                                                                                                                                                                                                                                             85 TAAAATCCCTTGTAAATCTTTTAAAACTCTTTTAAAATCCCTTGTAAATCTATTTCCCGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 TGTAAAAATAAACAAAACCTGTTATTTTTTTTTTTTAAGAAGGTAATCGGGAGACGTAG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 CAAAAAAAAAAATTGGGGGAAAATATGTTTGAAAACAAATTTTGGCGGGAAATTTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 GTATTTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTATACC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 GITTATATATAATTAGTGTAGAAAAATTTTTATTTAACCAGTCTTTTTTGGTCCC 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 2000;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERBUCE: 210121.52761
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                0; Mismatches 120; Indels
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PLILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 342 LENGTH: 338
                                                                                                                                                                                                                                             Score 38;
                                                                                                                                                                                                                                                                Pred. No
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                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aljun
APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.8%;
Matches 110; Conservative (
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Pred. No. 0.85;
0; Mismatches 69; Indels
                                                                                                        APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: 05/09/878,178
CURRENT FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
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                       Sequence 342, Application US/09878178 Patent No. US20020177552A1
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Best Local Similarity 53.4
Matches 79; Conservative
                                                                   GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
US-09-878-178-342/c
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-878-178-342
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LENGTH: 338
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App1:

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Run on:

Sequence:

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Sequence 132,
Sequence 11, A
Sequence 29, A
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: RECIPROCAL SUBTRACTION DIFFERENTIAL
TITLE OF INVENTION: DISPLAY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/032,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%; Score 157; DB 2; L/
100.0%; Pred. No. 9e-37;
ive 0; Mismatches 0;
                                                                                                    US-09-134-001C-135
JS-08-184-009-119
JS-08-458-356-119
JS-08-460-736-119
                                                                                                                                                                              -09-328-111-132
-09-461-474-11
                                                US-09-004-838-93
US-08-213-419B-3
US-07-924-028A-5
                                                                                                                                        -08-107-755A-8
-08-544-332-8
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                                                                                                                                                                  -09-370-861A-8
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US-08-334-639-1
                                      JS-08-213-419B-1
                                                                                                               US-08-232-463-14
                                                                                     US-08-078-090-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY, FATORNEY, FATORNEY, FACEDY I THORNATION:
REGISTRATION NUMBER: 28,678
REFERENCE, FOOKER INDHER: 5551/JPW/AMG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09032684 Patent No. 5882874
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 177 base pairs
TYPE: nucleic acid
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Matches 157; Conservative
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RY: USA
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ZIP: 10036
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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3-09-357-206A-20
3-09-357-206A-22
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US-08-117-083-23
US-08-117-083-67
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US-08-459-850-32
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US-08-257-073-2
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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                                                                                                                                  Title:
Perfect score:
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Minimum DB Maximum DB

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258 TIGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTC 317
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                                                                                                                                            378 TTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTTGCAGATCTGGGGGGT
                                                                                                                                                                                                                                                                                  498 TAGACCTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                           618 GGAGACGTAGGCAATAAAATGTTTTCAG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 376, Application US/09385982 Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(611)
; OTHER INFORMATION: n = A,T,C or
US-09-385-982-376
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Best Local Similarity 62.6'
Matches 107; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-385-982-376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 TTCCTCCCTAGGGCGGGGAAGCTGAGGTGCAGGGTTCAGACCCACGCGGCGAGCAGCTCTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 TGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Best Local Similarity 14.1%; Pred. No. 0.0066;
Matches 80; Conservative 214; Mismatches 274;
                                                                                                                                                                     Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: BCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                    744 GAAAATATTATGTTATGTAAAAAAAAAATCATGT 780
                                                                       121 GAAAATATTATGTTATGTAATAAAAAAAATCATGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELERAS: (703)835-4109
TELERS: 8991A
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: '435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149,
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATORNEZ/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNENCH: 7218 base pairs
TENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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1021 TGAGCGTATGGCAAACGAAGGAAAATAGTTATAGTAGCCGCACTCGATGGGACATTTCA 962
                                                                                          436 GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 GTTTCNGGTAAACNGGAAT-ATAANGNGAAAGAACAAACNTTGGAACATACTTAATGGAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITTIATAGACCTITGTAAACAAAAGGGGACTTGT-----TGAGAAGTCCTGTTTTATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 ITITATAGAACTITGNAAACCAAAGGAGATTCATGTTTTANAAGTCTGGCCCTTTTTATA 443
                                                         10;
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Pred. No. 0.029;
0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER PAPLICATION NUMBER: 09/328,111
EARLIER PELLING DATE: 1999-06-08
EARLIER PILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
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GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Datesh-Kumar, S.
APPLICANT: Barbara Barbara
APPLICANT: Barbara
APPLICANT: Barbara
APPLICANT: Barbara
APPLICANT: Barbara
BILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 ATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATTAAGTTAAAGGAC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACATGAAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTGAG 530
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                                              Vectors Encoding Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1500;
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREM: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 38; DB 1; Le
49.5%; Pred. No. 0.18;
tive 0; Mismatches 100;
                       Recombinant Virus Vector.
Papilloma Virus Proteins
: 70
                                                                                                                             ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-798-3249
Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531 AAGTCCTGTTTTTATACC 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1500 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                  APPLICANT: Munro, Alan J. TITLE OF INVENTION: Recon TITLE OF INVENTION: Papil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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Matches 98; Conservative
                                                                                 NUMBER OF SEQUENCES: 7(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                       CITY: San Francisco
STATE: CA
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US-09-357-206A-6/c
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                                                                                                                                         APPLICANT: Boursnell, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPENDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 720;
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Pred. No. 0.12;
0; Mismatches 100; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                          Sequence 23, Application US/08117083
Patent No. 5719654
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: BOUTSNELL, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
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Best Local Similarity 49.5%;
Matches 98; Conservative
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: CDNA US-08-117-083-23
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                                                   US-08-117-083-23
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US-09-357-206A-19/C
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SEQ ID NO 17
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Patent No. 6372962
GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REPERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR PILING DATE: 1998-07-20
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                                                                                                                                                                               390 TIGACATIGIATIGCIGCAAGATIAATGIGGTTIGCAGATCIGGGGGTATCIGGTAAACT 449
                                                                                                                                                                                                                                              450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTTATAGACCTTTG 507
                                                                                                                                                                                                                                                                                                            508 TAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAA 567
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                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: CDNA-N/intron construct: E1-E2-E3-I3-E4-E5 US-09-357-206A-16
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Pred. No. 0.64;
0; Mismatches 110; Indels
                                                                                                                DB 4; Length 1818,
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                                                                                                                                                                                                                                                                                                                                                                                                 568 IGTAAAAATAAACAAAACCIGITAITITITITITITTTAAGAAGGTAA 614
                                                                                                                                                0; Mismatches 110;
                                                                                                              Score 37;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 5253
 PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.7%;
Matches 115; Conservative (
                                                                                                              4.78;
                                               TYPE: DNA
ORGANISM: Nicotiana glutinosa
                                                                                                                             Best Local Similarity 50.79
Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-357-206A-16/c
                                1818
                                                                               US-09-357-206A-6
SOFTWARE:
SEQ ID NO 6
LENGTH: 181
                                                                                                                Query Match
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RESULT 8

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Sequence 17, Application US/09357206A
Patent No. 6372962
GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REFERENCE: 042250/194805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
FULCATION NUMBER: US/09/357,206A
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT PLILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: cDNA-N/intron construct: E1-11-E2-E3-13-E4-E5
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US-09-357-206A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.7%; Score 37; DB 4; Length 5483; 50.7%; Pred. No. 0.65; Live 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 37; DB 4; Length 5586;
50.7%; Pred. No. 0.65;
1ve 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3388 TAGACGAAATTATATTTTAAGTTAATTTTCTAATATTTAGGATTTTA 3342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 IGTAAAAATAAACAAAACCIGTTATTTTTTTTTTTTTAGAAGGTAA 614
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                               PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.7
Matches 115; Conservative
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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ORGANISM: artificial
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Matches 115; Conserv
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Score 37; DB 4; Length 6095; Pred. No. 0.68; 0; Mismatches 110; Indels

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4180 TIGAATTACGAGGCCAACACATTATTTTGIGIGAATATAGAAATTTATTTTTTATATA 4121
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                                                                              FEATURE:

OTHER INFORMATION: CDNA-N/intron construct: E1-E2-I2-E3-I3-E4-E5
US-09-357-206A-18
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Best Local Similarity 50.7%;
Matches 115; Conservative
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SOFTWARE: Patentin vi
SEQ ID NO 20
LENGTH: 6325
                                                         ORGANISM: artificial
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SEQ ID NO 18
LENGTH: 6095
                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dinesh Kumar, S.
APPLICANT: Baker, Barbara
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs FILE REPERBYCE: 042250/101805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
NUMBER OF FEC 1098-07-20
SOFTWARE: PatentIn version 3.0
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                                    3448 AAATTACAAAGGCTCTTAATGTCGTTCGTTTTTTTACCTTTAAAAATATTTTACAC 3389
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            450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTG 507
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; OTHER INFORMATION: cDNA-N/intron construct: E1-I1-E2-E3-I3-E4-I4-E5
US-09-357-206A-21
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Best Local Similarity 50.7%; Pred. No. 0.67;
Matches 115; Conservative 0; Mismatches 110;
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US-09-357-206A-18/C
; Sequence 18, Application US/09357206A
; Patent No. 6372962
; GENERAL INFORMATION:
; APPLICANT: Dinesh-Kumar, S.
; APPLICANT: Baker, Barbara
; TITLE OF INVENTION: Pathogen Resistant
                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09357206A Patent No. 6372962 GENERAL INFORMATION:
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GRUERAL INFORMATION:
APPLICAMT: Dinesh-Kumar, S.
APPLICAMT: Dinesh-Kumar, S.
APPLICAMT: Baker, Barbara
TITLE OF INVENTION: Parthogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REFERENCE: 04225/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/337,206A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
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4000 TAGACGAAATTATATTTTAAGTTAATTTTCTAATATTTAGGATTTTA 3954
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LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
US-08-261-663A-1
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                                   Sequence 22, Application US/09357206A
Patent No. 637296
Patent No. 637296
Patent No. 637296
APPLICANT: Dinesh Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs FILE REPERBNCE: 04226/191805 (5830-5)
CURRENT FILE OF DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US/09/357,206A
PRIOR APPLICATION NUMBER: US 60/093,494
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Patent No. 5571706
GENERAL INFORMATION:
APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
TITLE OF INFUNION: Plant Virus Resistance Gene and Methods NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 4; Length 6428;
Pred. No. 0.7;
0; Mismatches 110; Indels
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STREET: 800 Buchanan Street
CITY: Albany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,663A
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 50.7%;
Matches 115; Conservative
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 300
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ORGANISM: artificial
RESULT 13
US-09-357-206A-22/c
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SEQ ID NO 22
LENGTH: 6428
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4703 TIGAATTACGAGGCCAACACATTATITITGIGIGAATATAGAAATTIATTITITATATA 4644
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join(294..772, 1003..2098, 2941..3213, 5032..6600,
6934..6951)
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APPLICANT: Whitham, Steven A
TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; Length 7400;
Pred. No. 0.75;
0; Mismatches 110; Indels
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FT-10395-07754A-1/C
; Sequence 1, Application PC/TUS9507754A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                         ORGANISM: Nicotiana glutinosa
TISSUE TYPE: leaf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEPA: (510) 559-5777
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7400 base pairs
                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Best Local Similarity 50.7%;
Matches 115; Conservative
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MEDIUM TYPE: Floppy disk
                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double
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6601..6933
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773..1002
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390 TIGACATIGIATIGCIGCAAGATTAATGIGGITIGCAGATCIGGGGGTATCIGGIAAACT 449
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6934..6951)
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join(294..772, 1003..2098, 2941..3213, 5032..6600,
6934..6951)
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Pred. No. 0.75;
0; Mismatches 110; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07754A
                                                                ATTORING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CONDOT, MATGATE A
REGISTRATION:
NAME: CONDOT, MATGATE A
REGISTRATION NUMBER: 30043
REFERENCE/DOCKET NUMBER: 30043
TELEPHONE: (510) 559-6067
TELEPHONE: (510) 559-6067
TELEPKA: (510) 559-6067
TELEPKA: (510) 559-5777
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Nicotiana glutinosa
TISSUE TYPE: Leaf
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Best Local Similarity 50.7%;
Matches 115; Conservative
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6601..6933
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3214..5031
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773..1002
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Search completed: January 17, 2003, 02:02:32 Job time : 100 secs us-09-648-310-2.rag

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Human secreted pro
Arabidopsis thalia
Arabidopsis thalia
PSGen13 protein.
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                                                                                                                                    January 16, 2003, 21:51:23 ; Search time 143 Seconds (without alignments) 75.478 Million cell updates/sec
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1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD 81
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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QQQKQ44QKQQCKK4QCQ44Q444H.	AAG21477 AAG32488 AAG49689 ABB6463 ABB6473 AAB1287 AAB1287 AAB1287
ABBC27 ABB58 ABB58 AAB91 ABB92 AAB92 AAB92 AAB92 AAB92 AAB93	AAG AAB AAB AAB AAB AAB
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## ALIGNMENTS

Rat; Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer; blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon. Rat Progression Suppressed Gene 13 (rPSGen 13). AAU76532 standard; Protein; 81 AA. (UYCO ) UNIV COLUMBIA NEW YORK. 27-AUG-2001; 2001WO-US26795. 25-AUG-2000; 2000US-0648310. Su Z; (first entry) Fisher PB, Kang D, WPI; 2002-280914/32. N-PSDB; ABK11085. WO200216419-A2. 05-JUN-2002 28-FEB-2002 AAU76532; RESULT 1 AAU76532 

New rat and human Progression Suppressed Gene 13 for preventing the growth of cancer cells and/or new blood vessels, and for treating

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AAB56907:
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                                                                                                                  rat or human Progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer, c.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or be used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the amino acid sequence of rat progression Suppressed Gene 13 (rPSGen 13).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer; blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel isolated nucleic acids which encode a
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100.0%; Pred. No. 5.9e-46;
Live 0; Mismatches 0;
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patients suffering from a cancer
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                                                  Fig 1; 53pp; English
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Matches 81; Conserv
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Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
new blood vessels, and for treating patients suffering from a cancer, e-g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of the breast, lung, prostate, ovary or colon. PsGen 13 may also be used to suppress the transformed phenotype of a malignant cell. Administration of PsGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the maino acid sequence of human Progression Suppressed Gene 13 (HupsGen 13).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRKIVT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF15566 to AAF16505 encode the human prostate cancer associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 390; DB 23; Length 81;
Pred. No. 7.7e-44;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 1922; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB56907 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YPGELLLQGVHDDVDIILLQD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.18;
93.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAGELLLQGVHDDVDIVLLQD
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Best Local Similarity 93.8
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-587513/55.
                                                                                                                                                                                                                                                                                                                                                                                                        81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF16110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001
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polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, caradiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of genes AAC66410-C66458 encoding the human secreted proteins AAB32002-B32050. This sequence represents a fragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                             1 MNVEHEVNILVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                           Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein BLAST search protein SEQ ID NO: 114.
                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules encoding human secreted proteins,
                                                                                                                                                                                                       Score 390; DB 21;
Pred. No. 1.6e-43;
                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 387; 423pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB32056 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                        122 YPGELLLQGVHDDVDIILLQD 142
                                                                                                                                                                                                                                                                                                                                                     61 YAGELLLQGVHDDVDIVLLQD 81
                                                                                                                                                                                                     96.1%;
93.8%;
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99US-0171552.
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                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                   142 AA;
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22-DEC-1999;
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                                                                                                                               invention.
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and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases eg. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                           Length 83;
                                                                                                                                                                     1; Indels
                                                                                                                                           Score 375; DB 21;
Pred. No. 7.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                             Zea mays protein fragment SEQ ID NO: 76054.
                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                        AAG58854 standard; Protein; 87 AA.
                                                                                                                                           92.4%;
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                                                                                                                                                                                                                                        61 YAGELLLQGVHDDVDIVL 78
                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000 (first entry)
                                                                                                                                          Query Match
Best Local Similarity 93.6
Matches 73; Conservative
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                                                                                                                     83 AA;
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                                                                                               infections.
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                                                                                                                      Sequence
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	27-JUL-1999; 27-JUL-1999;	28-JUL-1999; 02-AUG-1999;	02-AUG-1999;	03-AUG-1999;	04-AUG-1999;	04 - AUG - 1999;	05-AUG-1999;	06-AUG-1999;	06-AUG-1999;	09-AUG-1999;	09-AUG-1999;	10-AUG-1999;	12-AUG-1999;	13-AUG-1999;	13-AIG-1999:	16-AUG-1999;	17-AUG-1999;	18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	25-AUG-1999;	26-AUG-1999;	27-AUG-1999;	27-AUG-1999;	27-AUG-1999;	30-AUG-1999;	31-AUG-1999;	01-SEP-1999;	07-SEP-1999;	10-SEP-1999;	13-SEP-1999;	15-SEP-1999;	16-SEP-1999;	20-SEP-1999;	22-SEP-1999;	23-SEP-1999;	26-SEF-1999;	20-CFD-1999.	04-00T-1000.	05-001-1999.	06-0CT-1999;	07-OCT-1999	08-OCT-1999;	12-0CT-1999:	13-0CT-1999;	13-OCT-1999;	13-0CT-1999;	14-OCT-1999;	14-0CT-1999;	14-0CT-1999;	14-0CT-1999;	14-0CT-1999;	18-0CT-1999;	21-OCT-1999;	21-OCT-1999:	21-0CT-1999;	21-0CT-1999;	21-OCT-1999;	22-OCT-1999;	22-OCT-1999;	22-OCT-1999;	25-OCT-1999;	25-OCT-1999;
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Length 83; Indels

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diabetes mellitus, Crohn's disease, multiple scierosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                 1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
   autoimmune haemolytic anaemia, autoimmune thyroiditis,
                                                                                                               70.4%; Score 286; DB 21; 70.5%; Pred. No. 4.6e-30;
                                                                                                                                        8; Mismatches
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99US-0128234
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                                                                                                                                        55; Conservative
                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                            Best Local Similarity
                                                                                       83 AA;
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     allergies,
                                                                                          Seguence
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antiacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of genes AAC66410-C66458 encoding the human secreted proteins AAB32002-B32050. This sequence represents a peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, homology search treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease,
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                                                                                                                                        Gaps
                                                                                                                                                              1 MNVEHEVNLLVEETHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
                                                                                                                                                                             Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers
                                                                                                                                        ;
                                                                                                               Length 87;
                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein BLAST search protein SEQ ID NO: 113.
                                                                                                                                       Indels
                                                                                                                                         13;
                                                                                                              Score 302; DB 21;
Pred. No. 3.7e-32;
'; Mismatches 13;
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                                                                                                                                                                                                                                                                                                     AAB32055 standard; Protein; 83 AA.
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                                                                                                               74.48;
74.78;
         990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161993.
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 99US-0161406
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                                                                                                                                        Conservative
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                                                                                                                           Similarity
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         26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                        28-OCT-1999
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25-OCT-1999
                                                                                                                           Best Local Sim
Matches 59;
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                                                                                                               Match
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
6 MNVDEEIQKLEEEIHRLGSRQTDGSYKVTFGVLFNDDRCANIFEALVGTLRAAKKRIVA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 75317.
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90S - 0135124 90S - 0135353 90S - 0135629 90S - 0136621 90S - 0136782 90S - 0137724 90S - 0137528 90S - 0137528 90S - 0137529	9 US - 0139453 99 US - 01394494 99 US - 01394455 99 US - 0139456 99 US - 0139456 99 US - 0139450 99 US - 0139461 99 US - 0139461 99 US - 0139461 99 US - 013961 99 US - 013961 99 US - 0140695 99 US - 0140695 90 US - 0140695	990S 014354 990S 014354 990S 0143654 990S 0144085 990S 0144086 990S 0144325 990S 0144334 990S 0144334 990S 0144334 990S 0144334 990S 0144334 990S 0144334 990S 0144336 990S 0145086 990S 0145086 990S 0145145 990S 0145145 990S 0145145 990S 0145145 990S 0145145 990S 0145145 990S 0145145 990S 0145145
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UGC -1999, 999 UGC -1	000 1999 999 999 999 999 999 999 999 999	SEP-1999; 9918 SEP-1999; 9918 SEP-1999; 9918 SEP-1999; 9918 SEP-1999; 9918 SEP-1999; 9918 CGT-1999; 9918	711099; 699
002,	10-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	2000 2000 2000 2000 2000 2000 2000 200	2011-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1

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99US-0145218.
99US-0145224.
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99US-0143624.
99US-0144005.
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99US-0144086.
99US-0144325.
99US-0144331.
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99US-0144632.
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99US-0145086.
99US-0145088.
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 990S-0136021.
990S-0136392.
990S-0136782.
990S-0137222.
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99US-0139750.
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                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                0; Gaps
                                                          Query Match 70.4%; Score 286; DB 21; Length 95; Best Local Similarity 70.5%; Pred. No. 5.5e-30; Matches 55; Conservative 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 75316.
                                                                                                                                                                                                         AAG58353 standard; Protein; 161 AA
 990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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990S-0123180.
990S-0123548.
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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28-APR-1999;
28-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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14-MAY-1999;
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PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147303.

PR 13-AUG-1999; 99US-014416.

PR 13-AUG-1999; 99US-014416.

PR 22-AUG-1999; 99US-014416.

PR 23-AUG-1999; 99US-0149368.

PR 23-AUG-1999; 99US-0149368.

PR 23-AUG-1999; 99US-0149368.

PR 23-AUG-1999; 99US-0149368.

PR 23-AUG-1999; 99US-0149323.

PR 24-SEP-1999; 99US-0151066.

PR 24-SEP-1999; 99US-0151066.

PR 25-AUG-1999; 99US-0151066.

PR 24-SEP-1999; 99US-015109.

PR 25-CCT-1999; 99US-01510
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This is the amino acid sequence of the PSGen13 protein (progression suppressed gene 13). PSGen13 has suppressed expression in progressed tumour cells. The PSGen13 nucleic acids sequence was identified using new tethods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction two samples. The method involves performing reciprocal subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed. The subtraction samples are amplified and compared to identify those with increased or reduced expression during tumour cell progression, e.g. progression suppressed genes (PSGen) and partern produced in conventional differential RNA display (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and coloning of genes displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified CDNA can be analysed by reverse Northern blotting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
                                                                                                                                                                                                                                                                                                                                                                                                                 Progression suppressed gene; PSGen; progression elevated gene; PEGen; tumour; reciprocal subtraction differential RNA display; RSDD; differential expression; gene cloning; cancer.
                                                                                                                               Gaps
                                                                                                           1 MNVEHEVNLLVEETHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
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                                                 Length 161;
                                                                               Indels
                                                                                15;
                                              70.4%; Score 286; DB 21; 70.5%; Pred. No. 1.1e-29;
                                                                             8; Mismatches
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                                                                                                                                                                                                                                                                                     AAY39325 standard; Protein; 92 AA
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98US-0197889.
99US-0161993.
99US-0162142.
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                                                                               Conservative
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                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                   PSGen13 protein.
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28-OCT-1999;
29-OCT-1999;
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23-NOV-1998;
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                                              Query Match
                                                              Best Local
Matches 5
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20000S-0232399
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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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                                                                                                                                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiathritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialheepic; antiidlacer; antilucer; anticonvulsant; antifungal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                         Gaps
                                                          Length 92;
                                                                                                                                                                                                                                       Human nervous system related polypeptide SEQ ID NO 3397.
                  Query Match 57.1%; Score 232; DB 20; Best Local Similarity 72.7%; Pred. No. 7.4e-23; Matches 48; Conservative 4; Mismatches 8;
                                                                                                                                                                         ABB14740 standard; Protein; 77 AA.
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2000US-0215135.
2000US-0216647.
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2000US-0220963
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92 AA
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                                                                                                   61 YAGELL 66
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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Sequence
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating comedical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haroimprist, diabetes mellitus, Crohn's callis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 3397; 1701pp + Sequence Listing; English.
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                                                                                          2000US-0249214,
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2000US-0249299
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Best Local Similarity
Matches 31; Conserv
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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L7-NOV-2000;
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05-DEC-2000;
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31-DEC-2000;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

WPI; 2001-639362/73. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

N-PSDB; AAS92182

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217 23-AUG-2000; 2000US-0649167

WO200175067-A2. Homo sapiens.

11-0CT-2001.

Claim 20; SEQ ID No 58354; 103pp; English.

biodiversity

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #27986.

18-FEB-2002 (first entry)

ABG27995;

ABG27995 standard; Protein; 456 AA.

RESULT 11 ABG27995

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colyperase chair reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The color identifying expressed genes. (I) is useful in gene therapy techniques (C restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or blological activity. C disponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cold sequences. Abg00010-Abg30377 represent novel human cut sequence data for this patent did not appear in the printed diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 DGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRKIVTYAGELLLQGVHDDVDIVLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 26.1%; Score 106; DB 22; Length 456; Local Similarity 43.1%; Pred. No. 2.8e-05; nes 25; Conservative 10; Mismatches 21; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Gaps

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MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGV 32 

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Conservative

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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w.tpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbial infection; antibacterial; Helicobacter pylori infection;
               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 6939; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73; DB 22; Length 399;
Pred. No: 0.54;
9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 EALVGILKAAKRRKIVTYAGELLLQGVHDDVDIVLLQ 80
                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB46383 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.0%;
                                                                                                                                                                               23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.
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                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
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    pylori HPC024 protein.

                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; screening
                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AA;
                                                                                                                                                                                                                                                                                                   N-PSDB; ABL04152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200073502-A2
                             pharmaceutical
                                                                                     WO200171042-A2
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                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA. sequences (ABL018176 ABL30511), expressed DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVNLLVEEIHRLGSKN-ADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGE
                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3420; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 6939.
                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 3420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%; Score 81.5; DB 22;
31.6%; Pred. No. 0.015;
ive 16; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB60049 standard; Protein; 399 AA.
                           ABB58876 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Li PWD,
                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.6 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 TLFOGRDDTEPVRLLR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 LLLQGVHDDVDIVLLQ 80
                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL02979
                                                                                                                                                                                                                         WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB60049;
                                                         ABB58876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
RESULT 12
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             ABB58876
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This invention describes a novel preparation of an agent (A) for detection, prevention and/or treatment of microbial infection by:

(d) identifying essential genes (I) and corresponding polypeptides

(II); (ii) identifying compounds that are directed against (II) and inactivate the microbe; (iii) testing these for suitability for use; and formulating selected (A). Identifying essential genes (I) comprises preparation of gene-deficient microorganisms by conditional antisense inhibition (CAI) and/or subtractive recombination mutagenesis (SRW).

The products of the invention have antibacterial activity. (A) (which may be a nucleic acid (Ia), vector or host cell containing (Ia), derived be a nucleic acid (Ia), vector or host cell containing (Ia), derived completed (IIa), or fragments, (IIa)-specific antibodies or their fragments or an inhibitor of (IIa) are particularly used for diagnosis, creatment or prevention of infection by Helicobacter pylori. Particularly contained (IIa) are used in DNA, subunit or live vaccines. The method infection by Helicobacter pylori. Particularly contained species, so identified (Ia) should have a broad spectrum of activity. Many energies, so identified genes can be used for screening without purification.
                                                                                                                          Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of essential genes in defective mutants -
                                                                     Meyer TF;
                                PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                    Hueck CJ,
                                                                                                                                                                       Claim 37; Figure 15; 366pp; German.
                                                                   Gibbs CP,
99DE-1027740.
                                             (CREA-) CREATOGEN GMBH.
                                                                  Apfel H, Fuchs TM,
                                                                                        WPI; 2001-049948/06.
N-PSDB; AAF25660.
                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA;
17-JUN-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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3 Gaps 3, Length 116; 24 GKLSVKFGVLFQDDRCANLFEAL-VGTLKAAKRRIVTYAGELLLQGVHD 72 Indels 21; Score 66.5; DB 22; Pred. No. 0.8; 6; Mismatches 16.4%; Query Match
Best Local Similarity 40.0°
Matches 20; Conservative ð

26 GGLFIGFVKVMQKDVLAQLMEHLETGYK--KREKTLAYMTKLLEGGIHE 73

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AAY91948 standard; Protein; 324 (first entry) 19-JUL-2000 AAY91948; RESULT 15 AAY91948 ID AAY9 

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Human cytoskeleton associated protein 3 (CYSKP-3).

Cytoskeleton associated protein; CYSKP-3; cancer; proliferative; autoimmunity; inflammatory, vesicle trafficking; neurological; cardiovascular; cell motility; reproductive; muscle disorder.

Homo sapiens

Location/Qualifiers

"potential phosphorylation site" "ankyrin repeat" "ankyrin repeat" "ankyrin repeat" /note= /note= 76..85 /notenote= Modified-site Domain Domain Domain

"potential phosphorylation site" "potential phosphorylation site" "potential phosphorylation site" 'note= "potential phosphorylation site" "potential glycosylation site" "potential glycosylation site" "potential phosphorylation phosphorylation phosphorylation phosphorylation "potential "potential "potential note. 81 note= /note= 289 /note= 304 'note= /note= 225 note= note= 'notenotenote= note= 'note= notenote-80 359 WO200017355-A2 Modified-site Modified-site

30-MAR-2000

99WO-US21565 17-SEP-1999;

98US-0172226 99US-0131321 18-SEP-1998; 27-APR-1999

(INCY-) INCYTE PHARM INC.

Corley NC; Bandman O, Baughn MR; Hillman JL, Azimzai Y, YT, Yue H, Patterson C, Tang Guegler KJ, Lal P,

WPI; 2000-283582/24. N-PSDB; AAA08583 Human cytoskeleton associated proteins, used to treat cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive and muscle disorders

Claim 1; Page 85; 113pp; English.

AAY91946-61 show human cytoskeleton associated proteins 1 to 16 (CYSKP-1 to CYSKP-16) respectively. The sequences can be used to treat and diagnose cancer and cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cardiovascular, call motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-16 can be used to treat or prevent disorders associated with decreased expression or activity of CYSKP (claimed), for example, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, cancers, autoimmune/antinflammatory disorders such as allergies, anemia, asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, diabetes mellitus, Goodpasture's syndrome, osteoarthritis, scleroderma and trauma. CYSKP antagonists can be used to treat or prevent a disorder associated with increased expression or activity of CYSKP (claimed).

Ą, 324 Sequence

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Query Match 16.0%; Score 65; DB 21; Length 324; Best Local Similarity 29.2%; Pred. No. 4.7; Matches 21; Conservative 11; Mismatches 30; Indels 10; Gaps
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	7 VNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRR 56   : ::   :	
3	T.F.	
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	FODE : XNOF	
ì	RLGSKNADGKLSVKFGVLFQD   :      :: :   HLDAKAADGNTALHYAALYNQ	
1	LSVK :: IALH	
1	DGKI	
3	SKNP :- I	
j	IRLG HLD	
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1	VNLLVE  :::: VDFIIQ	
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Q9nxk2 homo sapien Q8tdy4 homo sapien Q4391 acinetobact Q8xty1 pyrobaculum Q9xzM8 thermotoga Q9xq4 lutrzomyia 1 Q9zq96 arabidopsis Q21458 caenorhabdi

Run on:

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090XXZ
08PDY4
08PDY4
09WZMB
09XZM9
09ZQ96
09ZQ98
09ZQ98
09ZQ98
09ZQ98
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09ZQ98
09ZQ98
09ZQ86
00ZQ86
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 January 17, 2003, 02:00:53; Search time 114 Seconds (without alignments) 146.402 Million cell updates/sec
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                                                                                                                                      US-09-648-310-2
406
1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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sp_manmal:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
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Maximum DB seq length: 200000000
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115...
116...
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Perfect score:
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                                                                                                                                                                   Sequence:
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O95240 arabidopsis O92498 arabidopsis O92498 arabidopsis O92498 arabidopsis O92498 pelicobacte O92146 rhizobium m O9093 physarum po O87414 anabaena sp Q81811 thermoanaer O9711 ephydatia f O96068 ciona intes O96069 ciona intes O96068 ciona intes O96069 ciona intes O96068 ciona intes O96069 ciona intes O96068 ciona in

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*

sp\_archeap:\*

# SUMMARIES

	Description	O9cxu3 mus musculu	Ogplf3 homo sapien	09p0al homo sapien	081881 arabidonsis	062234 caenorhahdi	046052 drosophila	Ogyzw6 drosophila	022133 caenorhabdi	085431 rice strine	O980x3 mycoplasma	Ogopi4 campylobact	OBstof encephalito	Ogsrm7 arabidonsis	093w32 arabidonsis	O9sn36 arabidonsis	O9nxh7 homo sapien
	ID	Q9CXU3	Q9P1F3	Q9POA1	081881	062234	046052	09VZW6	022133	085431	Q980x3	09PPI4	OBSTP6	09SRM7	093W32	09SN36	O9NXH7
		1	4	4	10	2	2	2	S	12	16	16	S	10			4
	Query Match Length DB	81	81	141	161	162	371	183	289	2919	318	395	294	447	462	530	307
æ,	Query	99.3	96.1	96.1	70.4	23.8	20.3	20.1	20.1	17.5	17.0	16.9	16.6	16.6	16.6	16.3	16.0
	Score	403	390	390	286	96.5	82.5	81.5	81.5	71	69	68.5	67.5	67.5	67.5	99	65
1	NO.	н	7	3	4	S	9	7	8	6	10	11	12	13	14	15	16

RESULT Q9CXU3 ID O	JLT 1 U3 OSCXU3 PRELIMINARY: PRT: R1 AA
Y S	to 'IVI 'IVIII''' 'I'''''''''''''''''''''
텀	(TrEMBLrel. 17,
2 5	U1-UUN-ZUU1 (TrEMBLrel, 17, Last sequence update) 01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
DE	protein.
S C	SILOUOSAL/RIK. Mis misculis (Monse)
88	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ပွ	Rodentia;
×o	
N C	CROSTERIOR W. N.
5 2	CTDAIN-CATAL TOTACHE-ENDOVONIC DEAD.
RX	MEDLINE-21085660: Pubmed-11217851:
RA	Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
КA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
КĀ	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
R3	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
R.	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF.,
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ř	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA	Hayashizaki Y.;
RŢ	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
DR	EMBL; AK013984; BAB29100.1;
DR	MGD; MGI:1920362; 31100003A17Rik.

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Gaps

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**09P1F3** 

RESULT 2 Q9P1F3

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SEQUENCE FROM N.A.
Obermaler B., Deutschenbaur S., Piravandi E., Hoheisel J., Jesse T.,
Heijnen L., Vos P., Mewes H.M., Mayer K.F.X., Schueller C., Bevan M.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRKIVT 60
   Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.; "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF161398; AAF28958.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Obermaler B., Deutschenbaur S., Piravandi E., Mewes H.W., Lemcke
Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 286; DB 10; Length 161; larity 70.5%; Pred. No. 1.2e-25; Conservative 8; Mismatches 15; Indels (
                                                                                                                                                                                                                                                                                                                  Length 141;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALU31394; CAA200577.1; -.
EMBL; AL161583; CAB80081.1; -.
                                                                                                                                                                                                                                     7FD16DF8BC359EFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 161 AA; 18337 MW; 4F42A35D064DE8B5 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
14pothetical 18.3 Mas protein.
                                                                                                                                                                                                                                                                                                  Query Match 96.1%; Score 390; DB 4; Le
Best Local Similarity 93.8%; Pred. No. 6.4e-38;
Matches 76; Conservative 4; Mismatches 1;
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Last sequence update)
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                                                                                                                                                                                       NON_TER 1 1
SEQUENCE 141 AA; 15797 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 FEGELLLQGVHDKVEITL 144
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55; Conserv
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NCBL_TaxID=3702;
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01-AUG-1998
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                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                        1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapieńs (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    Score 403; DB 11; Length 81;
Pred. No. 9.4e-40;
1; Mismatches 0; Indels
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Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF116683; AAF71102.1; -.
EMBL; BC014953; AAH14953.1; -.
Hypothetical protein.
SEQUENCE 81 AA; 9056 MW; IFODCE7AlD22B171 CRC64;
   9058 MW; B444C508ACE602C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PR02013 (Hypothetical 9.1 kDa protein).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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93.8%;
                                                                        99.38;
                                                                                                       98.88;
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Best Local Similarity 93.8
Matches 76; Conservative
                                                                                                                                             Conservative
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   AA;
                                                                                                       Local Similarity
les 80; Conserv
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   81
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      Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Barrell B., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minana B., Kafaros F.C., Louis C., Siden-Klamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schottler P., Warner M., Mourkioti F., Beinert N., Dowe G., Schaffer U., Jackhe H., Bucheton A., Campbell L.A., Darlamitsou A., Henderson N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       optera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NVEHEVNLLVEEIHRLGSKNADG-KLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunder R.D., Glover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.8%; Score 96.5; DB 5; Length 162; Best Local Similarity 32.9%; Pred. No. 0.002; Matches 26; Conservative 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                  Cottage A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          C21116625BBF64B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0TN-1998 (TrEMBLrel. 06, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) F36F2.1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EG:152A3.3 protein (HL01173P).
EG:152A3.3 OR CG3630.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                          MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
BENEL; 281532; CAB04325.1;
SEQUENCE 162 AA; 18490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YAGELLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                              Caenorhabditis elegans.
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Ephydroidea; Drosophi
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                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                    NCBI_TaxID=6239;
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ralia J.F., Agbayani A., An H.-J., Badrataroglu L., Beasley E.M., Ballew R.M., Basca A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basca P.V., Bernan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borters K.C., Busam D.A., Burler H., Cadleu E., Center A., Chandra I., R. Burlis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., R. Burlis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., R. Burlis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Burlis K.C., Gabziellan K.J., Dayles E., Dourbe M., Dugal-Rocha S., Dunkov B.C., Dunn P., R. Dotson K., Doup L.E., Downes M., Dugal-Rocha S., Dunkov B.C., Dunn P., Burbin K.J., Exargelista C.C., Ferriera S., Fleischmann W., R. Goler C., Gabziellan A.E., Garg N.S., Gelbart W.M., Glasser K., Goler R., Gong F., Gorrell H.H., Gu Z., Gunn P., Harris M., Heuston K.A., Henland T.J., Wein M.-H., Ibegwam C., Almael B.E., Kodlar C.D., Kraft C., Kravittz S., Kull D., Lai Z., Askop P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Askop P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., McLeod M.P., Morphy D., Worlson D.M., Nelson D.L., Ra Alazkon D.R., Nolson K.A., Nixon K., Wuznker D.M., Nelson D.L., Radnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Radnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Radner S.M., Woodage T., Worley C., Wang S., Yang S., Yao O.A., Millams S.M., Woodage T., Worley C.M., Weissenbach J., Wang S., Wang S.-Y., Wars E.W., Rodonge T., Wolley K.C., Wang S., Zhu K., Smith H.O., R. Albeng R.A., Where E.W., Rubin G.M., Vehrer T., Saince L. Spradling A.C., Zhan M., Zhan G., Zhao Q., Zhao G., Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C.,
Champe M., Chavez C.,
Champe M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL009194; CAAL5697.1; --
EMBL, AR003423; AAL28541.1; --
EMBL, AYGOG993; AAL28541.1; --
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 RKIVTYAGELLLQGVHDDVDIVLLQ 80
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CG2113.
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RXARM-EBRIELEY;
RXARM-EBRIELEY;
RXARM-EBRIELEY;
RADAM-EBRIELEY;
RADAM-EBRIELEY
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Last annotation update)
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Best Local Similarity 31.6%;
watches 24; Conservative 1
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                                                                                                STRAIN-BERKELEY
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2465 MNGEIET----VEELNKLDKGFESHRLALVERIRVGKLGILGSYTKCQQRIEELDG---- 2516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-95088603; PubMed=7996149;

Toriyama S., Takahashi M., Sano Y., Shimizu T.;

Toriyama S., Takahashi M., Sano Y., Shimizu T.;

"Nucleotide sequence of RNA 1, the largest genomic segment of rice stripe virus, the prototype of the tenuivirus.";

J. Gen. Virol. 75:3569-3579(1994).

EMBL: D31879; BAR062138; Abl. Short.

InterPro; IPR002138; Abl. Short.
                                                                                                                                                                                                                                                                                           26; Indels 17;
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                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2919 AA; 336872 MW; 16FB7BC57FB12FC0 CRC64;
                                                                              Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                            investigating biology.";
Science 282:2018(1989)
EMBL: 235663: CAA84722.1;
SEQUENCE 289 AA: 32972 MW; 20DB67F731F03098 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice stripe virus (isolate T) (RSV).
Viruses; ssRNA negative-strand viruses; Tenuivirus.
NCBI_TaxID=36394;
                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                            Query Match 20.1%; Score 81.5; DB Best Local Similarity 33.7%; Pred. No. 0.23; Matches 29; Conservative 14; Mismatches.
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Rhabditidae; Peloderinae; Caenorhabditis
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
PROSITE; PS50802; OTU; 1.
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111 RKYGLVHFEGEMLYQRQDDEKIITML 136
                                                                                                                                                                                                                                                                                                                                                                                             54 KRRKIVTYAGELLLQGVHDDVDIVLL 79
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                                                                                                                                MEDLINE-99069613; PubMed-9851916;
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                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA polymerase.
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Q85431;
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Q98QX3;
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Q85431
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us-09-648-310-2.rspt

Length 395;

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MEDLINE-2012; PubMed-10688204;
MEDLINE-2012; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandraam M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                    Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDR-----CANLFE-----ALVGTLKAAK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
ou-ocT-2001 (TrEMBLrel. 18, Created)
01-oCT-2001 (TrEMBLrel. 18, Last sequence update)
01-oCT-2001 (TrEMBLrel. 18, Last annotation update)
Phosphate acetyltransferase (Phosphotransacetylase) (EC 2.3.1.8).
MYPU_2370.
                                                                                                                                                                                                                           "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Wucleic Acids Res. 29:2145-2153(2001).
BNBL; AL445563; CAC13410.1; -.
Mypuilst; MYPU_2370; -.
InterPro; IPR002505; PTA_PTB.
Pfam; PF01515; PTA_PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 69; DB 16; Length 318; 36.2%; Pred. No. 7.7; 1ve 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                              Transferase; Acyltransferase; Complete proteome.
SEQUENCE 318 AA; 35015 MW; ECE864ClAAB7E3EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45319 MW; 47237D2859DEB89E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative integral membrane zinc-metalloprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ninterPro; PR001915; Peptidase_M48.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01435; Peptidase_M48; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                          STRAIN-DAB CTIP;
MEDLINE-21267165; PubMed-11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Nature 403:665-668(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 RRKIVTYAGELLLQGVHDDV 74
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 36.23
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                           Mycoplasma pulmonis.
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                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE 395 AA;
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                                                                                                                  NCBI_TaxID-2107;
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09PPI4
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                                                                              2 NVEHEVNLLVEE-----IHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAK 54
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MEDIINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence and gene compaction of the eukaryote parasite Encephalitozon cuniculi."; Nature 414:450-453(2001).
EMBL; AL590451; CAD27101.1; -.
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBL_TaxID=6035;
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                                                                                                                                                                                                                                                                                                                                 ol-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein ECU09_1300.
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Last annotation update)
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16.9%; Score 68.5; D 26.2%; Pred. No. 12; ive 19; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last sem
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                                                                                                                                                         55 RRKIVTYAGELLLQGVHDDV
  Query Match 16.9%
Best Local Similarity 26.2%
Matches 21; Conservative
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nes 29; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamanura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
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                                                                                                                                                                                                                 17; Gaps
                                                                                sedneuce.";
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SEQUENCE FROM N.A.

STAINCY. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T19F11 genomic sequence."
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AC009918, AAF02137.1; ""H.G. Control of the Resciclin.
Interpro; IPR000782; B19H3_fasciclin.
Frou FROM STAIN T. SEQUENCE 447 AA; 49236 MW; B6CB1062AF267379 CRC64;
                                                                                                                                                                                                                                                           15 HRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGV 70
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                                                                                                                                                                                     Length 447;
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                                                                                                                                                                                 16.6%; Score 67.5; DB 10; Length 35.7%; Pred. No. 18; ive 8; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) AT3911700/T19F11_10.(Hypothetical 50.8 kDa protein) T19F11.10/AT3G11700.
                                                                                                                                                                                                                                                                                                                                                  462 AA
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                                                                                                                                                                                                                                                                                                                                                                                Created)
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462 AA; 50792 MW;
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Hypothetical protein.
SEQUENCE 462 AA; 50792 MW.
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                                                                                                                                                                                                              20; Conservative
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ses 20; Conserv
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Arabidopsis thaliana (Mouse-ear cress). Bukaryophyta; Tracheophyta; Eukaryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pittman J.K., Hall J.L., Williams L.E.;
"Identification of Nramp5, a heavy metal transporter in Arabidopsis
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;; Pred. No. 33;
11; Mismatches 36; Indels
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Mayer K.F.X.;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AL035526; CAB37464.1; -
EMBL; AL161949; CAB78881.1; -
EMBL; AJ292076; CAC27822.1; -
InterPro; IPR001046; Nramp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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PRODOM; PD01961; Nramp; 1.
TIGREAMS; TIGR01197; nramp; 1.
SEQUENCE 530 AA; 58781 MW; 837E2D22F1BB2E37 CRC64;
                                                                                                                                         Ion transporter-like protein (Heavy metal transporter). F28A21.200 OR AT4G18790 OR NRAMP5.
                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
530 AA
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a

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                                                  Fisher, P.B., Kang, D.C. and Su, Z.Z. Progression suppressed gene 13 (psgen 13) Patent: MO 0216419-A 5 28-FEB-2002; The Trustees of Columbia University in the
                                                                                                                                            100.0%; Score 780; Dilarity 100.0%; Pred. No. 5.5 Conservative 0; Mismatches
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/organism="Rattus sp."
/db_xref="taxon:10118"
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                   Chordata;
Rodentia;
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Rattus sp.
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Patent: WO 0216419-A 1 28-FEB-2002;
The Trustees of Columbia University
Location/Qualifiers
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/organism="Rattus
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                              Sattus norvegicus clone CH230-344I21, *** SEQUENCING IN PROGRESS ACI12858
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On Jul 14, 2002 this sequence version replaced gi:20162682.
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3. (bases 1 to 90548)
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                           AC117858.3 GI:21745767
HTG; HTGS_PHASE1.
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RESULT 3
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Center code: BCM

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
OVDE: This is a "vorking draft' sequence. It currently
consists of 44 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                             ' NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
------- Project Information
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NOTE: This is a "working draft" sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is
2 (bases 1 to 185634)
Worley,K.C.
Direct Submission
Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                Center project name: GNPS

Center clone name: CH30-143D2

Center clone name: CH30-143D2

Center clone name: CH30-143D2

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 124518 bases at least Q40

Consensus quality: 133171 bases at least Q30

Consensus quality: 139212 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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/protein_id="AAI.16773.1"
/db_xref="G1:16303307"
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FHTSRWYSLPFPWILKNNRFCLFYJWFCFRV"
159 c 108 g 226 t
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                            DB 10;
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                                                                                                                                                        Score 482.8; DB 10
Pred. No. 3.8e-117;
0; Mismatches 82;
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***, 108 unordered pieces.
AC105605
AC105605.2 GI:21743919
HTG; HTGS_PHASE1.
/product="unknown"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                 134350 AGATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 134291
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                                                                                              229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC
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1 (bases 1 to 692)
1 (bases 1 to 802)
1 (base) Angri, K. Yangri, E. and Reddy, P. K.
A novel CDNA clone from mouse thymus cDNA library
                  Score 550.4; DB 2;
Pred. No. 7e-135;
0; Mismatches 1;
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/db_xref="taxon:10090"
/tissue_type="thymus"
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                  70.68;
99.88;
              Query Match 70.6
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         1. (Dassel 1 to 294830)

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1. (Dassel 1 to 294830)

1. Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbard, J., Benton, J., Blange, K., Blanke, B., Brown, B., Drow, B., Carter, M., Cavazoos, S. R., Chacko, J., Drayd, R., Carter, M., Cavazoos, S. R., Chacko, J., David, R., David, R., David, M.L., Davis, C., Coy, C., Coy, Len, D., D., David, R., Douthwaite, K., Davy-Carroll, L., Dathorne, S. R., David, R., Douthwaite, K., Davy-Carroll, L., Dathorn, K.J., Douthwaite, K., Davy-Carroll, E., Dutbin, K.J., Douthwaite, K., Davy-Carroll, E., Davy-Carroll, R., Gancer, F., Rackotto, R., Garner, T., Garza, M., Gill, R., Capis, Gorteel, J., H., Gao, J., Garcle, A., Garner, T., Garza, M., Gill, R., Gabisi, A., Gao, J., Garcle, A., Garner, T., Garza, M., Gill, R., Harris, C., Harris, K., Huber, J., Haylak, P., Hawes, A., Hernandez, J., Howard, S., Huber, J., Huber, J., Jackson, L. E., Jacobson, B., Jai, Y., Johnson, R., Jollyet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, J., Khan, J., Kovar, J., Lu, W., Landry, N., Leal, B., Lewis, L.C., Kratcvic, J., Lucker, L., Landry, N., Leal, B., Lewis, L.C., Marshwarl, M., Maheshwarl, M., Maylou, P., Martin, R., Soctt, G., Shen, H., Shooshtari, N., Savery, G., Scher, S., Scott, G., Pale, R., Wang, S., Wartek, A., Tauber, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence Version replaced gi:18092828.

Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 108 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Dipublished

Stren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Boguslavkty, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chag, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kalls, C., LaRocque, K.,
Jones, C., Macdonald, P., Major, J., Marquis, M., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meltim, J.,
Mencus, L., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severty, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanlan, A., Tavis, N., Taillio, J., Yesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 21-AUG-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Petson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
                                -TTATTTTTTTTTTTTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAG
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Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Viel, R., Wola, Wilson, B., Wu, X., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

L Direct Submission

L Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061342.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: 118269
Center clone name: 191_F_12
Center clone name: 191_F_12
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 171878 bases at least Q40
Consensus quality: 174256 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 167000; agarose-fp
Insert size: 174483; sum-of-contigs
Quality coverage: 7.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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120 219: gap of 100 bp
220 1584: contig of 1365 bp in length
1585 1684: gap of 100 bp
1020 44019: contig of 42335 bp in length
1120 47141: contig of 3022 bp in length
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84: contig of 3685 bp in length
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47242 51149: contig of 3908 bp in length
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73488: contig of 7344 bp in length
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66044: contig
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Db 164344 AGATGCTGATGGAAAATTAAGTGTGAAGTTTGGGGTCCTCTTCCAGGATGACAGATGTGC 164403
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85.1%; Pred. No. 8.7e-91;
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                                /organism="Mus musculus"
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gap of 100 bp 37: contig of 11287 bp in length

83700: 95087

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95088

187: gap of 100 bp 109668: contig of 14481 bp in length

p of 100 bp contig of 19089 bp in length

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100 bp 22891 bp in length

contig of 22891

cont. 151848: cr.

28858 128957

51849 151948: gap of 100 bp 51949 175262: contig of 23314 bp in length

5362: gap of 100 bp 176083: contig of 721 bp in length.

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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Zamber, B., Zimmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Labbek, L., Simmer, A. and Zody, M.

Labbek, L., Zodo, Labbek, L., Cambridge, MA 02141, USA

On Aug 21, 2002 this sequence version replaced gi:17061622.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
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                           O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
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Center clone name: 69 K.2037,
Sequencing vector: Plasmid; now of reads
Sequencing vector: Plasmid; now of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 18153 bases at least 030
Consensus quality: 184245 bases at least 030
Consensus quality: 185286 bases at least 030
Insert size: 194000; agarose-fp
Insert size: 196170; agarose-fp
Usality coverage: 6.8 in 020 bases; sum-of-contigs
Quality coverage: 7.1 in 020 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
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contig of 1305 bp in length
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contig of 1782 bp in length
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20391: contig of 1717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p of 100 bp contig of 2613 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04: gap of 100 bp 24923: contig of 1719 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       966 1065: gap of 100 bp 1722: contig of 657 bp in length 1723 1822: gap of 100 bp 1823 1822: contig of 769 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               965: contig of 965 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp contig of 2170 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L18974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
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23104: cont
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12992 14773: cont
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8370: con
0: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16305 16404: gap of 16405 18574: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23204: gap of
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6928: cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
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1066 1722:
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JOURNAL
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State (199170)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Gooke, Y., Dearatlano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karlas, A., Kells, C., LaRocque, K., Lu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Morquis, N., Mathews, C., Macdonald, P., Major, J., Morphy, T., Naylor, J., Nguyen, C., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Multoy, R., Shencer, S., Schupback, R., Saman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Ye, W., Vo, A., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Lamer, A., and Zody, M., Lalams, V., Ye, Wyng, C., Wyng
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Mus musculus clone RP23-69K22, WORKING DRAFT SEQUENCE, 31 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 164818 TTCTGTCAAAGCAAGAAGCAACTGCAGACAGCTGCCATGAAAATGT--TGTTTATGG 164875
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 189170)
Db 164644 AGAAGTCCTGTTTTATACCTTGAAGCAAACATTACAATGTAAAATAAACAAAACC--- 164700
                                                                                                                                                                                                                                                                                                                                                                                  DD 164758 IGTGAAAAAGCTTTTGTTCTTTAAACCATTCTTAAGACAATTTCTACAGGCACTTGACA 164817
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                                                                                                                                                                                                                             164757
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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cook, P., Darzellano, R., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardya, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Liley, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Lindblad-Toh, K
                                                                                                                                                                                                                                                                                                                                      702
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                                                                                                                                                                D 164701 ---TATTATTTTTTTTTTAGAAGGTAATTGGGAAATGTAGGTAATGAAACATTTTTGGAGG
                                                                                                                                                                                                                                                                                                                           TGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTT-----AGTCTCTGCCACACTTGACA
                                                                                                         TTATTTTTTTTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGG
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AC102536.2 GI:22380841
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Birren, B., Nusbaum, C.
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SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

DEFINITION

RESULT 8 AC102536 ACCESSION VERSION KEYWORDS in length

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p of 100 bp contig of 3480 bp in length p of 100 bp contig of 43562 bp in length
                                                                                                                                                                                                                                                                                                                                                          .05143 105242: gap of 100 bp 120007: contig of 14765 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                           32166 132265: gap of 100 bp
32266 149030: contig of 16765 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           149031 149130: gap of 100 bp
149131 182946: contig of 33816 bp in length
203: gap of 100 bp
26589: contig of 1566 bp in length
899: gap of 100 bp
29318: contig of sess
                                                                                                                                                                                                                                                   84430: gap of 100 bp 88902: contig of 4472 bp in length 89002: gap of 100 bp 97203: contig of 8201 bp in length 97303: gap of 100 bp 105142: contig of 7839 bp in length
                                                   gap of 100 bp 18: contig of 2629 bp in length gap of 100 bp 49: contig of 2631 bp in length
                                                                                                                   49: gap of 100 bp 34373: contig of 2224 bp in length
                                                                                                                                                   p of 100 bp contig of 2615 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18247 183046; gap of 100 bp 183047 189170; contig of 6124 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP23-69K22"
/clone_lb="RPCI-23 Female Mouse BAC"
1. . . 965
/note="assembly_fragment
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/note="assembly_fragment"
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16405. .18574
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029. .8370
note="assembly_fragment"
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note-"assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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26690. .29318
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/organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                      con.
J: gap of
40668:
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84330: cont
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37088: con
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                                                                                                                                  Db 142161 AGAFGCTGATGGAAAATTAAGTGTGAAGTTTGGGGTCCTCTTCCAGGATGACAGATGTGC 142220
                                                                                                                                                                                  Db 142341 AGATTAATGTGGTTTGCATGGCTTGGTGTATCTGATAACTGGAATAACTAAGTTAAAAG 142400
                                                                                                                                                                                                                                                                                                                                                                                                                     142460
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fisher, P.B., Kang, D.C. and Su, Z.Z. Progression suppressed gene 13 (psgen 13) and uses thereof Patent: WO 0216419-A 3 28-FEB-2002; The Trustees of Columbia University in the City of New York (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CICCGICAAAGTGAGAAGCGAACIAAAGACCAACIGCGGIGGAAAAIAIIAIGITIAIGI 762
                                                                                                                229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 288
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                                                                                                                                                                                                                                                  GTACGCAGGAGGTGCTTTTGCAAGGTGTTCATGATGATGTTGACATTGTATTGCTGCA
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                                                    Length 189170;
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                                                  49.3%; Score 384.2; DB 2;
llarity 85.1%; Pred. No. 8.7e-91;
Conservative 0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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Pred. No. 5.6e-78;
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/note="assembly_fragment"
29419. .32049
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/organism="Homo sapiens"
/db_xref="taxon:9606"
160 c 176 g 253
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Sequence 3 from Patent WO0216419.
AX456992
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                                                                Local Similarity
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Best Local Similarity
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                   misc_feature
                                                                               Matches 469;
                                                  Query Match
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AX456992
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16

Matches

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522 536 582 969

5

Gaps

255

195 222

162

315

375 402 462

641 655

581 595 713

761

source

REFERENCE AUTHORS

JOURNAL FEATURES

TITLE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS

RESULT 10 AX456995

762

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HTG 10-APR-2002
SAMPLING.
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Mus musculus clone RP23-383F11, LOW-PASS SEQUENCE SAMPLING.
AC117670
AC117670.1 GI:20128437
HTG; HTGS_PHASE0.
Mus musculus.
Mus musculus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutherla; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                   283 ATTIGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAAC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGG 435
                                                                                                                                      TGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCCTCCCTAGGGCGCGGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGCAGCTC 135
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                                                                                                                        136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT
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                                                                    Length
                                                                                              Indels
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Pred. No. 5.6e-78;
0; Mismatches 218;
                             u
                            253
/organism="Homo sapiens"
/db_xref="taxon:9606"
160 c 176 g 25
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                                                                  43.0%;
llarity 69.1%;
Conservative
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539; Conserv
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Best Local
Matches 53
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KEYWORDS
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                         BASE COUNT
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Primates; Catarrhini; Hominidae; Homo.
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 Gaps
                                                                             TGTTCCTCCCTAGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGCAGCTC 135
                                                                                                                                                                                        CCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAA 255
                        Fisher, P.B., Kang, D.C. and Su, Z.Z. Progression suppressed gene 13 (psgen 13) and uses thereof Patent: WO 0216419-A 6 28-FEB-2002;
The Trustees of Columbia University in the City of New York
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                                                                                                                                                                                                                                                          283 ATTIGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAAC
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                                                                                            136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT
                                                                                                                                                CCGCCGGGAAGGAAAACCGCGCAGAGAGCAATGAATGTGGATCACGAGGTTAACCT
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 Mismatches
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Sequence 6 from Patent WO0216419,
AX456995
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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11667 11166; gap of 100 bp 1167 11166; gap of 100 bp 11862 19616; gap of 100 bp 12747 12746; gap of 100 bp 13520 14202; contig of 683 bp in length 13520 14202; contig of 681 bp in length 14303 14993; contig of 691 bp in length 15094 15093; gap of 100 bp 14993; contig of 691 bp in length 15885 15884; contig of 661 bp in length 15885 16645; gap of 100 bp 16855 16645; gap of 100 bp 16855 16645; gap of 100 bp 16895 16645; gap of 100 bp 16895 16930; contig of 699 bp in length 17335 17434; gap of 100 bp 16831 19930; contig of 699 bp in length 18132 18930; contig of 699 bp in length 19731 19620; gap of 100 bp 18231 19630; contig of 673 bp in length 19721 19620; gap of 100 bp 18232 13822; gap of 100 bp 20593; gap of 10
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                                                                                                                                                                                                     Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chango, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Daaz, J.S., Dodge, S., Gard, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gordte, M., Garbam, L., Grand-Pierren, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Mayuen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nail, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, R., Santos, R., Schauer, S., Schupback, R., Stauss, N., Subramanlan, A., Tavis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Johnsell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Son, P., Volel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Son, P., Volel, R., R., R., R., R., L., Santos, M., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Son, P., Coon, P., Coon
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Center clone name: 383_P_11
                                                                                                Mus musculus, clone RP23-383P11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 GAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATTG 398
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698 bp in length
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52115: contig of 702 bp in length
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53814 53813: gap of 100 bp
53814 54499: contig of 686 bp in length
54500 54599: gap of 100 bp
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contig of 693 bp in ap of 100 bp in contig of 685 bp in ap of 100 bp in contig of 675 bp in ap of 100 bp in contig of 684 bp in
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40240: contig of
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                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 107625; contig of 107625 bp in length

* 10726 107725; gap of 100 bp

* 111442 111541; gap of 100 bp

* 111442 111541; gap of 100 bp
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                                                                                                                                                                                                     Insert size: 170000; agarose-fp
Insert size: 170482; sum-of-contigs
Quality coverage: 13.6 in 020 bases; sum-of-contigs
Quality coverage: 13.6 in 020 bases; sum-of-contigs
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                               reads
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120164 161248: contig of 41085 bp in length
161249 161348: gap of 100 bp
161349 170882: contig of 9534 bp in length.
Location/Qualifiers
                                                                                                                        Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consenus quality: 169805 bases at least 030 Consenus quality: 169800 bases at least 030 Consenus quality: 170139 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 334.2; DB 2;
Pred. No. 1.6e-77;
0; Mismatches 43;
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37012 c 37190 g 44751 t
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/note="assembly_fragment"
111542. .120063
/note="assembly_fragment"
120164. .161248
/note="assembly_fragment"
                                                                                                               Summary Statistics
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clone_end:SP6
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/clone="RP23-284K1"
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89.4%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarhini; Hominidae; Homo.
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beljing Taiping Road 27, Beljing 100850, P. R. China
                                                                                                                                                 56383
                                                                                                                                                                                                                                                                                                        TATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATT 458
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1-876
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
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219 TGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACG 278
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/note="predicted protein of HQ2013"
/product="PRO2013"
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09-MAY-2001 (Rel. 67, Last updated, Version
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/organism="Homo sapiens"
/clone="FLB7547"
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Query Match

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: a Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7959862. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MNYDHEVNLLVEEIHRLGSRNADGKLSVKFGVLFRDDKCANLFE
ALVGTLKAAKRRIVTYPGELLLQGVHDDVDIILLQD"
106 c 157 g 221 t
                                                                                                                                                                                                                                                                                                                                                                           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hslao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dunnes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                  Direct Submission
Submitted (01-007-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
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                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDN Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
DNA Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Blood, natural Killer cell"
/clone_lib="NIH_MGC_106"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein PRO2013"
/protein_id="AAH14953.1"
/db_xref="G1:15928977"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:58527"
/db_xref="taxon:9668"
/clone="MGC:22978 IMAGE:4849571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.3%; Score 283.4; DB 69.0%; Pred. No. 3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: poTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
    Eukaryota; Metazoa;
                                             (bases 1 to 743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 485; Conservative
                                                                                                                                                                                                                                                                                                                                        BC Cancer Agency,
info@bcgsc.bc.ca
                                                                 Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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/protein_id="AmF71102.1"
/translation="MNVDHEVNLLVEEIHRLGSKNADGKLSVKFGVLFRDDKCANLFEA
LVGTLKAAKRRRIVTYPGELLLQGVHDDVDIILLQD"
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Homo sapiens, hypothetical protein PRO2013, clone MGC:22978
IMAGE:4849571, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446
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                                                                                                                                                                                                          42 TITCICITAGCCCGAACCACTICCTICTTCTGCTTGTTCCTCCCTAGGGCGCGGGAAGCTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGTTTCTGGTAA 427
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                   682 TAGTCT--CTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGC
                                                                                                                                                                                                                                                 TTTTTTTTTGCCTCAGCCACTTCCTTGGCCTCACCCTCCCCAGTGCACTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                           GGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCCTTCCAAGACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGGAATAATTAAGTTAAAGGACAAACAT --- GAAGTTCCTTATGTATTTTATAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITGTAAACAAAAGGGGA--CITGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 AATCTATGTATGATGCTATAAAATAAATCCTATTATTTTTCTCAGGAATCTGGTTAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTTACGTACGCAGGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCT
                                                                                                                                                                     23;
                                                                                                                         DB 17; Length
                                                                                                                                                                     Indels
                                                                                  BP; 333 A; 131 C; 167 G; 245 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTA------
                                                                                                                                                                   0; Mismatches 211;
                                                                                                                                               Pred. No. 4.7e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGAAAATATTATGTTATGTAATAAAAAA 773
                                                                                                                       41.1%; Score 320.4;
69.0%; Pred. No. 4.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC014953
BC014953.1 GI:15928976
                                                                                                                                                                   Conservative
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                                                                                                                                           Best Local Similarity
Matches 520; Conserv
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ORGANISM

RP11-501K14 is from the library F of Pieter de Jong. For further de http://www.chori.org/bacpac/home.vBCTOR: pBACe3.6 IMPORTANT: This sequence is not t RP11-501K14 It may be shorter bet sections only once, except for a returned left end of clone RP11-3 The true left end of clone RP11-3 The true left end of clone RP1-3 The true left end of clone RP1-3 The true right end of clone RP1-3 The true right end of clone RP1-3 The true right end of clone RP1-3 Coration Qualifiers    1.00296	// / / / / / / / / / / / / / / / / / /		/note="Limm8 repeat: matcher repeat_region   1051.   11550   repeat_region   11051.   11350   repeat_region   11051.   11350   repeat_region   1361.   12691   repeat_region   12850.   13009   repeat_region   15295.   13141   repeat_region   15295.   15341   repeat_region   15442.   15341   repeat_region   15442.   15441   repeat_region   15441   repeat_region   15442.   15441   repeat_region   15441
GAAGGAAGTTCTAACATATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGTTG ACATTGTATTGT	553 AGCAAAACATACAAAATAAAAAAAACCTGTTATTTTTTTT	AL590308  AL590308  Human DNA sequence from clone RP11-501K14 on chromoson sequence.  AL590308  AL50308  AL50308	chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGF/Chr6
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SULT CUS CUS CUS CUS CESS CESS CESS ONGA OURCE ONGA OUTTH JOUR	

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the entire insert of clone a 100 base overlapping a 100 base overlap. 1-501R14 is at 1 in this sequence. 225E12 is at 98297 in this sequence. 1-94L3 is at 97304 in this sequence.
RPCI-11.2 constructed by the group details see e.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atches 2242. .2323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atches 2242. .2317 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tches 5114. .5126 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atches 5863. .6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atches 5126. .5867 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tches 129. .279 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nes 2607. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nes 1768. .1916 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atches 45. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atches 90. .281 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tes 2587. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tches 21. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                               ches 103. .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atches 2. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atches 3. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thes 194. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nes 962. .2419 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ches 142. .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ches 21. .166 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atches 1. .79 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ches 14. .151 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nes 821. .962 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thes 97. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ches 7. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tt 100% conserved"
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7052...27421
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29709...2861
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30862...31350
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31350...31897
                                                                                                                                                                                                                                                                                                                                                                      /evidence-notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91. .444 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2351, .2547 of consensus"
2027, .22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note="AluJb repeat: matches 1. .297 of consensus"
23321. .22369
10104="L2 repeat: matches 2547. .2593 of consensus"
2394. .22607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6229. .16532
note="AluSx repeat: matches 1. .301 of consensus"
6577. .16796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2749 of consensus
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85384. .35496
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/note="MIR repeat: matches 32. .147 of consensus"
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                                                                                                                                                                                                                                                                         .149 of consensus"
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note-"6 copies 8 mer gaaagaaa 79% conserved"
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// Anote-*MER46C repeat: matches 82. .191 of
21843. .22026 --- matches 2351. .2547 of c
                                                                                                                                                                                                  .88 of
                                                                                                                               .217 of
                                                                                                                                                                                                  Anote="MER58C repeat: matches 40. 18586. 18687
Anote="MIR repeat: matches 48. 1
19512. 20572
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fnote="L2 repeat: matches 2667.
23146. .23213
                                                                                                                       /note="MER20 repeat: matches 1.
18247. .18407
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34911. .35200
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2674, .22981
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/note="7 copies 8 mer tccttcct 75% conserved" 37227. 37266 mer tccttcct 75% conserved" 37227. 37271. 37269 mer tccttcct 75% conserved" 38122. 38421 matches 211. 250 of consensus" 700te="Alusx repeat: matches 11. 310 of consensus" 700te="12 repeat: matches 2616. 2717 of consensus" 700te="Aluso repeat: matches 4. 310 of consensus" 700te="Aluso repeat: matches 4. 310 of consensus" 700te="THEIA repeat: matches 1. 353 of consensus" 7014="THEIA repeat: matches 1. 353 of consensus" 41414. 41703
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The WashU-HHMI Mouse EST Project
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//lab_host="DHIUDH"
//lab_host="Vector: pSPORTI; Site_1: Not I; Site_2: Sal I; Five libraries representing EI0.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library bNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram fingle-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library laserts and hybridized to an Ecot of 6. Single-stranded (unhybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite
                      Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marrah, V., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Teagareishvili, R., Williams, T. Endocrine Pancreas Consortium
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (brownefas harvard.edu)
MGI:1948459 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
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Other_ESTs: id05d03.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Pred. No. 2e-104;
0; Mismatches 42
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Best Local Similarity 92.0%;
Matches 504; Conservative
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                         REFERENCE
                                                            AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases I to 593)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                    AA544950 593 bp mRNA linear EST 04-AUG-1997 vk38e06.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:948898 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:545754
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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/dev_stage="4 weeks"
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EST 20-DEC-2001
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0271-10 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
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1 (bases 1 to 600)

White, R.A., Bershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Bersmand, P.D., Thomas, T.L., Gan, L. and Klein, W.H. Gene expression in the developing mouse retina by EST sequencing and microarray analysis

Nucleic Acids Res. 29 (24), 4983-4993 (2001)

21671835

Contact: Klein WH
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/clone_lib="Mouse E14.5 retina lambda 2AP II Library"
/tissue_type="neural retina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117; 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
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bily1389 551 bp mRNA linear EST 12-MAR-2002 id05d03.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5662133 5' similar to TR:081881 081881 BI791389
/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGACTG----, Other
information regarding entire library may be found at
thtp://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies htm "
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                                                                                                                          vm41a03.rl Knowles Solter mouse blastocyst Bl Mus musculus cDNA aA607954
                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 613)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: embryo; Vector: pSPORT; Site_1: Not!;
Site_2: Sal1; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: Sal1(dT):
5'-CGGTCGACCGTCACCGTTTTTTTTTTTTTT-3'. cDNAS were
cloned into the Not1/Sal1 sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:564996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 AAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTG 287
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/tissue_type="blastocyst"
/de_stage="embryo (pre-implantation)"
/lab_host="bH10B"
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                             724 ACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA 773
                                                The Washu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Wouse EST Project
Washington University School of Medicinep
Washington University School of Medicinep
Tel: 314 286 1810
Fax: 314 286 1810
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0; Mismatches 72;
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/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="texon:10090"
/clone="IMAGE:992716"
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Location/Qualifiers
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591 bp mRNA linear EST 30-JUL-1997
vj80b03.rl Soares_mammary_gland_NbkMG Mus musculus cDNA clone
IMAGE:035309 5', mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Martin,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                      648 GTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTT ---- AGTCTCTGCCACACTTGAC
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Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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/db_xref="taxon:10090"
/clone="IMAGE:935309"
/clone_lib="Soares_mammary_gland_NbMMG"
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Location/Qualifiers
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                                                       T 3'); double-stranded conA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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uw52c09.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3465616 3' similar to TR:081881 081881 HYPOTHETICAL 18.3 KD
BE687862
BE687862.1 GI:10075486
          pT7T3D-Pac (Pharmacia
                                                 2,
         /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmaci) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                      Score 455; DB 9; Length 593;
Pred: No. 5.8e-104;
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/lab_host-"DH10B"
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88.5%;
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Matches 51
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/sex="female (latting)"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT73D-pac (Pharmacia) with a modified
/note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
00 a 145 c 95 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                              Project (CGAP),
                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1384976
High quality sequence stop: 389.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249
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1 (bases 1 to 669)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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/clone_llb="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.9%; Score 452; DB 10;
ilarity 85.4%; Pred. No. 3.2e-103;
Conservative 0; Mismatches 80;
                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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551 489 ORGANISM

KEYWORDS SOURCE

TITLE JOURNAL

COMMENT

AUTHORS REFERENCE

359 491

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BE689324 504 bp mRNA linear EST 11-SEP-2000 uw52c09.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3465616 5' similar to TR:081881 081881 HYPOTHETICAL 18.3 KD
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                     CTTGTTCCTCCCTAGGGCGCGCGGAAGCTGAGGGGTTCAGACCCACGCGGCGAGCAGC 133
                                                                                                                                                                                                                          TCTTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAAC 193
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               Pred. No. 4.8e-94;
); Mismatches 51; Indels
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High quality sequence stop: 4
Location/Qualifiers
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Unpublished (1997)
Other_ESTs: uw52c09.x1
         89.28;
                                            494; Conservative
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            Best Local
Matches 49
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/clone="IMAGE:5710372"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

This. clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , is GTGCGTGGAA. This ilbidity we construct the Date of Date of Idea Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ445291 547 bp mRNA linear EST 29-MAY-2002
UI-M-ERO-bxn-b-05-0-UI.rl NIH_BMAP_ERO Mus musculus cDNA clone
IMAGE:5710372 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 547)
                                                                                                                                                                                                                                         ATTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTATACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .547
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                                                                                                                                                                                                                                                                                                                                     GGAGCAAAACATTACAATG 569
                                                                                                                                                                                                                                                                                                                                                                        GAAGCAAACATTACAATG 507
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source

FEATURES

Query Match

BASE COUNT ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 507)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)

L Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Eax: 314 286 1810

Email: mouseest@atson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 CTGCTTGTTCCTCCCTAGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGC 130
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                                                                                                                                                                                                                                                           Seq primer: ETPrimer
High quality sequence stop: 359.
Location/Qualifiers
1..507
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone="lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507;
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clone IMAGE:439056 5', mRNA sequence.
                                                      (Pharmacia
                                                                                                                                                                                                                                                               ë
                                                /note="Organ: mammary gland; Vector: pr7T3D-Pac (Pharmac ) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                                                                                                                                                                                                                342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642
                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGITGAGAAGTCCTGTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 583 AACCTGTTATTTTTTTTTTTTTAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                          TTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGGTCCTCTTCCAAGACGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATTAAGT
                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                 Length 591;
                                                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                 ; DB 9;
2.1e-96;
            /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                             167 t
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                 Score 425;
Pred. No. 2.
                                                                                                                                                                                            143 g
                                                                                                                                                                                                                                 54.5%;
88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA008262.1 GI:1464233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||| ||||| TGGAGGTGTGAAAGCCTT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 CAGAGGTGCGAAAAAGCTT 661
                                                                                                                                                                                             o 96
                                                                                                                                                                                                                                           Best Local Similarity 88.7
Matches 496; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
Mus musculus
                                                                                                                                                                                          185
                                                                                                                                                                                                                                 Ouery Match
                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                         223
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AA008262
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KEYWORDS
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Genome Res. 6 (9), 791-806 (1996)
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ORIGIN
                   JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                         FEATURES
                                                    COMMENT
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                                                                                           /note="Vector: pu7T3D-pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF468668
UI-M-BH3-atu-a-11-0-UI.rl NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-atu-a-11-0-UI 5', mRNA sequence.

BF468668.1 GI:11537851
                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 501)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                               337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAG 517
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 GACAGATGTGCCAATCTCTTTGAAGCGTTGGTAGGAACTCTGAAAGCTGCAAAACGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATT
                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                       DB 10; Length 504;
                                                                                                                                                                                                                                                                                                    Indels
/db_xref="taxon:10090"
/clone="IMAGE:3465616"
/clone_llb="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                     53.2%; Score 414.6; DB 10;
llarity 91.6%; Pred. No. 8.6e-94;
Conservative 0; Mismatches 40;
                                               /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAAAACCTATTATTTTTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAAAACCTGTTATTTTTT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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BF468668
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/db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone="UI-M-BH3-atu-a-11-0-UI"
/clone="UI-M-BH3-atu-a-11-0-UI"
/clone="II-M-BH3-atu-a-11-0-UI"
/clone="II-M-BH3-Atu-a-11-0-UI"
/clone="II-M-BH3-Atu-a-11-0-UI"
/dev_stage="17-32 days"
/lab_host="DT-32 days="DT-32 days="DT-32
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                                                                                                                                                                                                                                    Email: mEST@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS.
should be noted that Bento Soares is generating a small number o
additional specialized non-redundant arrays of BMAP cDNNs whose
availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TTCTGCTTGTTCCTCCCTAGGGCGCGGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAACTGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 GCAGCTCTTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Indels
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Pred. No. 1.5e-93;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.0%;
91.8%;
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Best Local Similarity 91.8
Matches 448; Conservative
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/note="Organ: heart; Vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://dsun.grc.nia.nih.gov/cDNA) Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA linear EST 01-FEB-2002 CDNA Library Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 580)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                    313
                                                                                                                                                                          TGCAAGGTGTTCATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGA 428
TTAACCTCCTGGTGGAGGAAATTCATCGCCTGGGTTCCAGAAATGCTGATGGAAAATTAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnad[gsun.grc.nia.nih.gov
Plate: L0506 row: D column: 12
Seq primer: -21M13 Forward
                                                    Systematic Analyses of NIA Mouse Newborn Heart cDNA Library
Unpublished (2001)
                                                                                                                     GTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIA Mouse Newborn Heart cDNA Library"
/tissue_type="Newborn Heart"
/dev_stage="Newborn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="niaEST:L0506D12-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                             BM122169 580 bp
L0506D12-3 NIA Mouse Newborn Heart
clone L0506D12 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM122169.
BM122169.1 GI:17105937
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BM122169/c
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with Sali and NotI enzymes, and cloned into Sali and NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with ligation mixture by the chemical method. The average insert size is about 1.8 kb. The library was constructed by than Piao (NIA)."
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                                                                                                                                              205 GGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGT
                                                                                                                                                                                                         TTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTA
                                                                                                                                                                                                                                                                                                                                                                                                     GACAATTTCTACAGGCACTTGACATTCTGTCAAAGCAAGAAGCAAACTGCAGACCAGCTG
                                                                                                                                                            CCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGC
                                                                                                                                                                                                                                           CGCAAAACGAAGGAAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGA
                                                                                                                                                                                                                                                                                           385 TGATGTTGACATTGTATTGCTGCAAGATTAAATGTGGTTTGCAGATCTGGGGGTATCTGGT
                                                                                                                                                                                                                                                                                                                                         445 AAACIGGAATAATTAAGITAAAGGACAAACAIGAAGITCCITAIGIAITITIAIAGACCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     683 ----AGTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGGGAACTAAAGACCAACTG
                                                                                                                        14;
                                                                                               Length 580;
                                                                                               Score 406.6; DB 13; Length
Pred. No. 8.8e-92;
0; Mismatches 69; Indels
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                                                                                              tch 52.1%;
al Similarity 85.6%;
492; Conservative
                                                             Ø
                                                            177
                                                                                              Query Match
Best Local S
Matches 492
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2.56 g of total RNA. The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal3 (include Sal1 sequence). The CDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, CDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the CDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with Sal1 and Not! enzymes. Then, the CDNAs were cloned into Salze Fractionation Column. The CDNAs were cloned into Salz/Not! site of pSPORT! plasmid vector. The DH10B E. col! host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan plao."
                                                                                                                                                  Losses 1 to 672)
Tanaka, T.S., Janaka, Sciurognathi; Muridae; Murinae; Mus.
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Dol, H., Wood, W.H.
III, Becker, K.G. and Ko, M.S. H.
Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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AW555045 672 bp mRNA linear EST 31-AUG-2000 L0249C06-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA clone L0249C06 3', mRNA sequence.
                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0249 row: C column: 06
Seg primer: -21M13 Forward
High quality sequence stop: 672
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xrefe="nia559:10249C06-3"
/db_xrefe="taxon:10090"
/clone="10249C06"
/clone=1ib="NIA Mouse Newborn Ovary cDNA Library"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 15;
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Pred. No. 2.3e-109;
0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Newborn Ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .672
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Contact: George J. Kargul
                                                  AW555045
AW555045.1 GI:7200468
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86.4%;
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Best Local Similarity 86.4
Matches 577; Conservative
                                                                                                       house mouse.
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                          /protein_id="Bab29100.1"
/db_xref="G1:12851587"
/db_xref="HGD:MG1:1920362"
/translation="NNVEHEWNLIVEIHRIGSRNADGKLSVKFGVLFQDDRCANLFE
ALYGTLKAAKRRKIVTYAGELLLQGVHDDVDIVLLQD"
                                                                                                                                                                                                                                                                          5
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Pred. No. 3.6e-125;
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                                                                                                              746. .751
/note="putative"
769
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146 c 174
                /codon_start=1
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86.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kondo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tamaka, T., Matsuura, S., Kakai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK013984 769 bp mRNA linear HTC 19-JAN-2002
Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
library, clone:3110003A17:homolog to PRO2013, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                     624
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TAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTTAG
                                                                                                                                                                                                                                                                                                                                                                            TCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAAGACCAACTGCGGTGG
                                                        AAACTGGAATAATTAAGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTATAGACCT
                                                                                                                               TTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTA
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High-efficiency full-length cDNA cloning
Wath. Enzymol. 303, 19-44 (1999)
99279253
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, W., Gastalov, S., Casavant, T. Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrind, L.M., Stabuli, F., Stauki, R., Tomita, M., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninoi, P., de Bonaldo, M.F., Brownstein, M., Bult, C., Fletcher, C., Fujita, M., Gariboli, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of sequence [5' GAGAGAGATTAATTAAATTACCCCCCCCCCC 3'], cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
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/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/note="data source:SPTR, source key:Q9P1F3, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/db_xref="MGD:MGI:19106054"
/db_xref="taxon:10090"
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                                                                                                                                                                                /dev_stage="adult"
//dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-pec (Pharmacia) with a modified
polylinker: Site_1: Not I: Site_2: Eco RI; The UI-R-DR1
library is a normalized Rat Osteoblast library (nREO)
constructed in pT3T7 vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag AAGATATCAA between the Not I cloning site and
dT18 stretch. The Rat Osteoblast Lissue was provided by
Lian & Stein of the University of Massachussetts Medical
tail. The sequence tag present in the cDNA between the NotI site and the Oilgo-dT track served to verify it as a clone from the normalized osteoblast library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: MI3 Forward
POLYA-Yes
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Pred. No. 4.7e-152;
0; Mismatches 5;
                                                                                                                                                          /clone="UI-R-DR1-ckz-m-14-0-UI"
/clone_lib="UI-R-DR1"
                                                                                                                   /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                230
                                                                                                                                  /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-R-DR1
TAG_TISSUE=osteoblast
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163 c 109 g
                                                                                          Location/Qualifiers
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Best Local Similarity 99.0%;
Matches 661; Conservative
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AA891725 642 bp mRNA linear EST 08-JAN-1999 EST195528 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKIAGO2 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                      Lie, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J., Karlavage, A. R. and Adams, M. D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
Onpublished (1998)
On Apr 3, 1998 this sequence version replaced gi:3018604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_l: EcoRI;
Site_2: NotI"
155 c 99 g 204 t
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               GTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAA
                                                                             92 GTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA
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9712, Medical Center Drive, Rockville, MD 20850, USA
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/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RKIAG02"
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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AA916139
AA712021
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AA91639
BM596390
AI234233
AA916399
BM712682

## RESULT

ALIGNMENTS

AW492391 BG164526 AW027019

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BQ192542/c	
LOCUS	BQ192542 690 bp mRNA linear EST 30-APR-2002
DEFINITION	1 Rattus norvegicus
	UI-R-DR1-ckz-m-14-0-UI 3', mRNA sequence.
ACCESSION	BQ192542
VERSION	BQ192542.1 GI:20368093
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norveqicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 690)
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
	discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Soares, MB
	Program for Rat Gene Discovery and Mapping
	University of Iowa
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA
	Tel: 319 335 8250
	Fax: 319 335 9565
	Email: msoares@blue.weeq.uiowa.edu
	The sequence contained an oligo-dr track that was present in the
	oligonucleotide that was used to prime the synthesis of first
	strand cDNA and therefore this may represent a bonafide poly A

Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.

em\_gss\_other:\*

em\_gss\_hum:'

em\_gss\_pln: em\_gss\_inv:

em\_gss\_pro:\* em\_gss\_rod:\*

,	Description	BQ192542 UI-R-DR1-	AA891725 EST195528	AK013984 Mus muscu	AW555045 L0249C06-	BG804701 0271-10 M	BI791389 id05d03.y
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                               Query Match
Best Local Similarity 67.5%; Pred. No. 1.1e-20;
Matches 154; Conservative 0; Mismatches 74; Indels 0;
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146 GCCATGAACGTGGAGGAGGAGGTCGGGAGGCTCAAGGAGGAGATCCATAGGCTCGGCCAG 205
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                                                       287 GCCAATCTTTGAAGCGTTGGTGGAACTCTGAAAGCCGCAAAACGAAGAAGATGTT 346
                                                                   227 AAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGT
                             Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 75315.
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0; Mismatches 79; Indels
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267 TCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGCCG 326
             270 CTCTTTCCGTGATGATAAATGTGCCACCTCTTTGAAGCATGGTAGGAACCCTTAAAAGCTG 329
                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                                                                               Zea mays DNA fragment SEQ ID NO: 76053.
                                AAC53910 standard; DNA; 551 BP
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99US-0136021
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99US-0136782
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                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                           Zea mays subsp. mays.
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
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05-MAR-1999;
09-MAR-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
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28-APR-1999;
30-APR-1999;
30-APR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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25 - MAY - 1999;
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11-MAY-1999
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08-NOV-2000;
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(ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycocardial ischaemias; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infectious diseases such as viral, bacterial, fungal and parasitic infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AGGGCGCGCAAGCTGAGTGCAGGGTTCAGACCCACGGGCGAGCAGCTGTTCAGTGAAGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 73; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 351 BP; 104 A; 72 C; 103 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.0
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-541565/60.
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                                                                                                                                                                                                                                                       06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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AAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCC 266

207 210

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nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive, antiinflammatory, anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antiidiabetic; antiinflammatory; antiiallergic; antiidiabetic; antiidiabetic; antiidiabet; natiincenausant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss
    260 AAATGCTGATGGAAAGTTAANTGTGAAAATTGGGGTCCTCTTTCGTGATGATAANTGAGC 319
                                         Human nervous system related polynucleotide SEQ ID NO 73.
                                                                                                                                                                                        ABAll066 standard; cDNA; 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01334
                                                                                                                                                                                                                                                                            23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                    ABA11066;
                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomdulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibadies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes: The proteins may also be used to prevent disorders, such as for system disorders, muscular disorders, immune system disorders, immune system disorders, immune system disorders, immune system disorders, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated proteins,
                                                                                                                                                                                                          identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AATGAACGIGGAGCAIGAGGITAACCICCIGGIGGAGGAAAIICAICGICIGGGIICCAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAIGCCGAIGGGAAACIGAGIGIGAAGIIIGGGGICCICTICCAAGACGACAGAIGIGC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                            Human colon cancer antigen nucleotide sequence SEQ ID NO:318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 388 BP; 109 A; 70 C; 95 G; 84 T; 30 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC97991 to AAC98763 encode the human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 764; 2104pp; English.
               AAC98308 standard; cDNA; 388 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US05883.
                                                                                                09-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                WO200055351-A1.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Matches 156;
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                                                           AAC98308;
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                                                                                                                                                                                      Human;
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AAC98308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a fragment of the progression suppressed gene 13

(PSGen13). This gene has suppressed expression in progressed tumour

cells. PSGen13 was identified using new methods for identifying nucleic

acids differentially expressed between two samples. The method involves

performing reciprocal subtraction differential RNA display (RSDD) between

the two samples to generate two subtraction samples. The subtraction

samples are amplified and compared to identify those nucleic acids that

are differentially expressed. The method is used to identify and clone

differentially expressed genes, particularly those nucleic acids that

are differentially expressed genes, particularly those incleic acids that

ceduced expression during tumour cell progression, e.g. progression

cuppressed genes (PSGen) and progression elevated genes (PEGen). The

method reduces the complexity of the band pattern produced in

conventional differential RNA display (where bands may be obscured,

resulting in false positive signals) since most bands common to both

samples are eliminated, alformatial mentodial progression and cloning of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
663 TGTTTTCTTAAACCATTCTTAGTCT -- CTGCCACACTTGACACTCCGTCAAAGTGAGAAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified cDNA can be
                                                                                       Progression suppressed gene; PSGen; progression elevated gene; tumour; reciprocal subtraction differential RNA display; RSDD; differential expression; gene cloning; cancer; ss.
                                                                                                                                            721 CGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA 773
                                                                                                                                                                   20.1%; Score 157; DB 20; Length 177; larity 100.0%; Pred. No. 2.5e-34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment of progression suppressed gene 13 (PSGen13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 177 BP; 72 A; 28 C; 30 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysed by reverse Northern blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examples; Fig 23; 110pp; English.
                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLUMBIA NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0032684.
                                                                                                                                                                                                                                                                                      AA221551 standard; DNA; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US04323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0185115
98US-0197889
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DYCO ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fisher PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus sp.
                                                                                                                                                                                                                                                                                                                              AAZ21551;
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identification; reciprocal subtraction differential display;
    683
                                                                               743
                                                                                               684 GTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTG 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of isolating and identifying differentially expressed nucleic acids between two samples by using a reciprocal subtraction differential display (RSDD) method. This sequence represents clone PSGen-13 which is a novel gene.
GTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTTA
                    GTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying differentially expressed nucleic acids between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 177 BP; 72 A; 28 C; 30 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.1%; Score 157; DB 20;
100.0%; Pred. No. 2.5e-34;
ive 0; Mismatches 0;
                                                                                                                                                                           744 GAAAATATTATGTTATGTAAAAAAAAAATCATGT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAATATTATGTTATGTAATAAAAAAATCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by reciprocal subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Fig 23; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                           AAX25869 standard; cDNA; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0032684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0032684
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation; identification;
RSDD; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Clone PSGen-13 sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-214060/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                        08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5882874-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fisher PB;
                                                                                                                                                                                                                                                                                                                                 AAX25869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624
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RESULT 12

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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribosyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 GCCGCAAAACGAAGGAAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 CATTTTTTGTTTCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAAACATTTGAACATACT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TCTGGTAAACTGGAATAATTAAAGGTTAAAGGACAAAACAT ---GAAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 TAATGTATTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGCCTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 TTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIATGIATITITATAGACCTITGIAAACAAAGGGGGA - - CITGITGAGAAGTCCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.5%; Score 206.6; DB 24; Length 68.7%; Pred. No. 4.4e-48; ive 0; Mismatches 144; Indels
       Human; colon tumour; vaccine; colon cancer; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 552 BP; 190 A; 104 C; 75 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 939; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Xu J,
                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                                                                                                                                                                                                            31-JUL-2001; 2001WO-US24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 68.7
Matches 366; Conservative
                          immunotherapy; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                  Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-241739/29.
                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                   WO200212328-A2.
                                                                          Homo sapiens.
                                                                                                                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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                                                                                                                                                                                                                                                                                                                                                                                                                             expressed in cancer tissues. ABB78993 to ABB78004 represent proteins expressed in cancer tissues. ABB78993 to ABB78004 represent proteins encoded by the AB8060776 to AB8060787 nucleic acid sequences. (1) can be encoded by the AB8060776 to AB8060787 incleic acid sequences. (1) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (1) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (1) in a cell. A probe/primer derived from (1) can be used for determining the presence of a nucleic acid which hybridises to (1), and for determining the phenotype of cells in a sample of cells from a patient. (1) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate maroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (1) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGCCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386
                                                                                                                                                                                      Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAACGAAGGAAGATTGTTACGTACGCAGGAGCTGCTTTTGCAAGGTGTTCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGITGACATTGTATTGCTGCAAGATTAATGTGGTTTTGCAGATCTGGGGGGTATC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%; Score 215.6; DB 24; Length 627; ilarity 83.3%; Pred. No. 1.3e-50; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 627 BP; 171 A; 151 C; 153 G; 147 T; 5 other;
                                                                                                                                                                                    Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA encoding colon tumour protein, SEQ ID
                                                                                                                                                                                    Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 796pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK45388 standard; cDNA; 552
                                           02-OCT-2001; 2001WO-US30732.
                                                                                        02-OCT-2000; 2000US-237271P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                            Thiaglingam A, Lewis ME;
                                                                                                                                                                                 Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 245; Conservat
                                                                                                                                                                                                                                                     WPI; 2002-426115/45.
                                                                                                                                      (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2002
11-APR-2002
                                                                                                                                                                                    Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK45388/c
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                                     73 GCTTGTTCCTCCTAGGGCGCGCGAAGCTGAGTGCAGGGTTCAGACCCACGCGGGGGAGCAG 132
                                                                                192
                                                                                           92 TCTCCGGCGGBABGBAAACGCGCGABAGAGGCAGCAATGAATGAATGAGGGTCACGAGGTTAA 151
                                                                                                                        252
                                                                                                                                                                312
                                                                                                                                                                                   271
                                                                                                                                                                                                       372
                                                                                                                                                                                                                                           AGGTGTTCATGATGATGATGATGATTGCTGCAAGATTAATGTGGTTGCAGGATCTG 432
                                                                                                                                                                                                                                                                                     476
                                                                                                                                                                                                                                                                                           391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molino GA;
                                                     133 CTCTTCAGTGAAGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAA
                                                                                                                                CCTCCTGGTGGAGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGT
                                                                                                                                                                                                    GGGGTA-------TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT-
                                                                                                                                                             GAAGTTTGGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; cancer; tissue profiling; forensic; mapping;
genetic analysis; diagnostic; antisense therapy; gene; ss.
                      19;
   Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        related nucleotide sequence SEQ ID NO:748.
                                                                                                                                                                                                                                                                                                                                   Dwivedi P,
                    93; Indels
                                                                                                                                                                                                                                                                                                                      477 --GAAGTTCCTTATGTATTTTATAGACCTTTGTAAACAAAAGGGGACT
 Score 252.2; DB 2
Pred. No. 6.8e-61;
0; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 796pp; English
32.3%;
76.1%;
                                                                                                                                                                                                                                                                                                                                                                                             ABQ57053 standard; cDNA; 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000; 2000US-237271P
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                  Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgess C, Astle JH,
Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER CORP.
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200229086-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon
                                                                                                                                                                                                                                                                                                                                                                                                               ABQ57053;
 Ouery Match
                                                                                                                                                                                212
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB7893 to ABB79004 represent proteins encoded by the ABQ60775 to ABB760787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoractive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and concleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate acroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise attibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                 TGTTCCTCCCTAGGGCGCGCGAAGCTGAGGGGTTCAGACCCACGCGGCGAGCAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTGGGGTCCTCTTCCAAGACGACAAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGAAAGCCGCAAAACGAAGGAAGATGTTACGTACGCAGGAGGAGCTGCTTTTGCAAGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTCATGATGATGTTGACATTGTATTGCTGCAA - - GATTAATGTGGTTTGCAGATCTGG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCGGGAAGGAAAACCGCGCAGAAGGAAGGAATGAATGTGGATCACGAGGTTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT
                                                                                                                                                                                                                                                                                                        DB 24; Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer related nucleotide sequence SEQ ID NO:557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; cancer; tissue profilling; forensic; n
genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                       Sequence 717 BP; 192 A; 171 C; 155 G; 180 T; 19 other;
                                                                                                                                                                                                                                                                                                      Score 250.4; DB 24;
Pred. No. 2.2e-60;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                    32.1%;
ilarity 75.6%;
Conservative (
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ID ABQ56862 standard; cDNA; 627
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                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 323;
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345 TCTTAAAGCTGCAAAAACGAAGGAAGATTGTAACATATCCAGGAĠAGCTGCTTCTACAAGG 404
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                                                                                                                                                                                                                                          AAC66413 standard; DNA; 712 BP.
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99US-0171552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
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                                                                                                              436 GTATC 440
                                                                                                                                                465 GTACC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                14-FEB-2001
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                                                                                                                                                                                                                                                                              AAC66413;
                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymorlectide encoded by a nucleic acid which hybridises to (I) in a cell. A probe-primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in the presence of a nucleic acid which hybridises to (I) is useful for determining the presence of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
                                                                                                                                                                                                                                                                                                                Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTCCTCCTCCTCCAGCCGTCTTTCTCTTTGCCTCAGCCACTTCCTTGGCC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 TGTTCCTCCCTAGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGCAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid that is differentially expressed in cancer
tissues useful for determining the presence of colon cancer in a cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGGGGTCCTCTTCCAAGACGACACAGTGTGCCAATCTCTTTGAAGCGTTGGTGGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 ATTIGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 CCGCCGGGAAGGAAACCGCGCAGAGAAGCAGCAGTGATGATGTGGATCACGAGGTTAACCT
                                Human; colon cancer; cancer; tissue profiling; forensic; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysis, mapping and diagnostic applications. (I) can be used tantibodies, and to screen for peptide analogues and antagonists.
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0
Human colon cancer related nucleotide sequence SEQ ID NO:750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%; Score 263; DB 24; Length 594; 76.0%; Pred. No. 5.6e-64; Ive 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                Dwivedi P,
                                                     genetic analysis; diagnostic; antisense therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 594 BP; 157 A; 142 C; 134 G; 149 T; 12 other;
                                                                                                                                                                                                                                                                                                              Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                          or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                            Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 796pp; English.
                                                                                                                                                                                                                                                                                                              Carroll
                                                                                                                                                                                                  02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                    02-OCT-2000; 2000US-237271P
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Matches 323; Conservative
                                                                                                                                                                                                                                                                                                            Astle JH,
A, Lewis
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP
                                                                                                                                                                                                                                                                                                            Burgess C, Ast
Thiaglingam A,
                                                                                                                           WO200229086-A2
                                                                                         Homo sapiens
                                                                                                                                                               11-APR-2002
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The invention relates to the isolation of genes AAC66410-C66458 encoding 49 human secreted proteins AAB32002-B32050. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or tradiing medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital: (b) immune discretase e.g. Addison's disease, allergies, autolumune haemolytic anaemla, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collises, collisis, (c) cardiovascular disorders such as myocardial ischaemlas; (d)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonussant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
376 TGTTCATGATGATGATGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein coding sequence SEQ ID NO: 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 336; 423pp; English.
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Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                       641
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                                                                                                                                                                                                                                                                               642 ATTITCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGCAGGGAT 701
                                                                                                                                                                                                                                                                                                                                                     761
                                                                                                                                                                                                                                                                                                                                                                                714 TGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAAA 773
                                                                                                                                                                                                                                                                                                                                                                                               Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
343 TCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGG
                                                                                                                                            AAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGACT--TGTTGAGAAGTC
                              376 IGTICATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGG
                                           TTTTTTTTTTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAA
                                                                                                                                                                                                                                                                                                                       AAGCTTTTGTTTTCTTAAACCATTCTTAGTCT - - CTGCCACACTTGACACTCCGTCAAAG
                                                                                                                                                                                                                                                                                                                                                  GGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAG
                                                                                      GTA---------TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---G
                                                                                                                                                                         ACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGT
                                                                                                                                                                                                     CTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAACAAAACCTGTTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer antigen nucleotide sequence SEQ ID NO:545.
                                                                                                                                                             Claim 1; Page 1004-1005; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF16110 standard; cDNA; 778 BP
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(ROSE/) ROSEN C A.
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proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                 disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
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                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 TTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT
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                                                                                                                                                                                                                                                                       DB 21; Length 778;
                                                                                                                                                                                                                                                                   Score 288.2; DB 21; Length
Pred. No. 5e-71;
2; Mismatches 167; Indels
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                                                                                                                                                                                                                                  Sequence 778 BP; 250 A; 151 C; 148 G; 221 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                  Query Match 36.9%;
Best Local Similarity 69.9%;
Matches 451; Conservative
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                   Gaps
                                     9
                                           AGTICCTTATGTATTTTATAGACCTTGTAAACAAAGGGGACTTGTTGAGAAGTCCTG
                                                                                                                                                                                   CTTCCTTCTTCTGCTTGTTCCTCCCTAGGGCGCGGGAAGCTGAGTGCAGGGTTCAGACCCA
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                                                                                                      CGCGGCGAGCAGCTCTTCAGTGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGA
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                                                                                                                                          GCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAATGCCGATGG
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   Length 800;
                   Indels
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  20;
         .3e-202;
  DB
                  0; Mismatches
 Score 754.8;
Pred. No. 1.3
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tch 96.8%;
al Similarity 99.5%;
778; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 TGTTCCTCCCTAGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGGGGAGCAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TTCAGTGAAGAAGGAAGCAATCGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT 195
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                                                                                                                       /product= "Progression suppressed gene 13 protein"
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blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                              New rat and human Progression Suppressed Gene 13 growth of cancer cells and/or new blood vessels,
                                                                         Location/Qualifiers
197..442
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                              patients suffering from a cancer
                                                                                                                                                                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 2; 53pp; English
                                                                                                                                                                                                                                                    25-AUG-2000; 2000US-0648310.
                                                                                                                                                                                                                     27-AUG-2001; 2001WO-US26795
                                                                                                                                                                                                                                                                                                                   Kang D,
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                                                                                                                                                        WO200216419-A2
                                              Homo sapiens
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                                                                                                    The invention relates to novel isolated nucleic acids which encode a rat or human Progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer, cancer of the breast, lung, prostate, ovary or colon. PSGen 13 may also be used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour mass, number of cancer cells, serum tumour marker, tumour improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of rat Progression
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                                       New rat and human Progression Suppressed Gene 13 for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCACGAGCTCTCCTCGTCCCCTTCTCCACTGCAGCCTTTCTCTTTAGCCCGAACCA
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                                                                                                                                                                                                                                                                                  DB 24; Length 780;
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                                                                                                                                                                                                                                                            Sequence 780 BP; 223 A; 151 C; 187 G; 219 T; 0 other;
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                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 780; DB 24 Best Local Similarity 100.0%; Pred. No. 1e-209; Matches 780; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                      Suppressed Gene 13 (rPSGen 13).
                                                                                  2; Fig 1; 53pp; English,
         2002-280914/32
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                   P-PSDB; AAU76532
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has suppressed expression in progressed tumour cells. PsGenil was identified using new methods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction differential RNA display (RSDD) between the two samples to generate two subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed. The method is used to identify and clone differentially expressed genes, particularly those with increased or reduced expression and progression elevated genes (PEGen). The method reduces the complexity of the band pattern produced in conventional differential RNA display of the bands common to obth samples are eliminated, allowing identification and cloning of genes displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the progression suppressed gene 13 (PSGen13). This gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
                                                          720
                                                                                                                     780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGen;
                             TTTGTTTTCTTAAACCATTCTTAGTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAG
                                                                                                                     /product= PSGen13
/note= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Progression suppressed gene; PSGen; progression elevated tumour; reciprocal subtraction differential RNA display; differential expression; gene cloning; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Progression suppressed gene 13 (PSGen13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Fig 35B; 110pp; English.
                                                                                                                                                                                                                                                                                                                                             BP
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98US-0185115.
98US-0197889.
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Novel CDNA sequenc Novel CDNA sequenc Corn tassel-derive Corn tassel-derive Human secreted pro Chemically treated Human gene regulat Chemically treated

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Rat; Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer;
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ABN94189
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/SIDS2/gcgdata/geneseq/genesegn-emb1/NA1981.DAT:
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                     Gaps
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Geiser J.R., van Tulnen D., Brockerhoff S.E., Neff M.M., Davis T.N.;
"Can calmodulin function without binding calcium?";
Cell 65:949-959(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87028234; PubMed-3533275;
Davis T.N., Urdea M.S., Masiarz F.R., Thorner J.;
"Isolation of the yeast calmodulin gene: calmodulin is an essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93278279; PubMed-1304352; Brockerhoff S.E., Edmonds C.G., Davis T.N.; Schonds C.G., Lavis T.N.; Structural analysis of wild-type and mutant yeast calmodulins by limited proteolysis and electrospray ionization mass spectrometry. Protein Sci. 1:504-516(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Sąccharomycetaceae; Saccharomyces.
NCBI TaxID=4932; .*
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5A5507544E06184C CRC64;
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01-JAN-1988 (Rel. 06, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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14; Mismatches
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                                                                                                                                                                                  DNA replication; ATP-binding; Helicase.
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                                                                                                                              EMBL; X83413; CAA58369.1;
InterPro; IPR003840; Herpes_helicase.
Pfam; PF02689; Herpes_Helicase; 1.
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MEDLINE-87228267; PubMed=3295478;
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                                                                                                                                                                                                                                           93286 MW;
                                                                                                          EMBL; U13194; AAA68468.1; -. EMBL; X83413; CAA58369.1; -.
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Best Local Similarity 23.00,
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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PTM: THE N-TERMINUS IS BLOCKED.
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                                                                                                                                                                     J. Blochem. 119:1045-1055(1996).
-!- FUNCTION: CALMADOULIN MEDIATES THE CONTROL OF A LARGE NUMBER OI ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROPEIN KINASES AND
                     MEDLINE=96424985; PubMed=8827436;
Ohki S.-Y., Miura K., Saito M., Nakashima K.-I., Maekawa H.,
Yazawa M., Tsuda S., Hikichi K.;
"Secondary structure and Ca(2+)-binding property of the N-termina
half domain of calmodulin from yeast Saccharomyces cerevisiae as
studied by NMR.";
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Pred. No. 6.8;
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Job time : 81 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ||: ::| || | |::
100 LISAAELKHVLTSIGEKLTDAEVDDM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 TLKAAKRRKIVTYAGELLLQGVHDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD; S0000313; CMD1.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 4.
ProDom; PD000012; EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M14760; AAA34504.1; -. EMBL; X78993; CAA55612.1; -. EMBL; Z35978; CAA85064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.7%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF_HAND;
Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
NMR OF 1-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A25060; MCBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
CA_BIND
CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            This :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                          - ADP + N-acetyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-95266321; PubMed-7747482;
Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathlou S., Craxton M., Macaulay H.A.;
Martin M.E., Efstathlou S., Craxton M., Macaulay H.A.;
Martin D.A. sequence of human herpesvirus-6: structure, coding content,
and genome evolution.";
Virology 209:29-51(1995).

-:- FUNCTION: THES PROTEIN MAY BE AN HELICASE AND IS REQUIRED FOR
REPLICATION OF VIRAL DNA.

-:- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 ULS,
EHV-1 57, EBV BBLF4, HCMV ULIO5, AND VZV 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes.";
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osynthesis; Transferase; Kinase; Complete proteome.
257 AA; 27810 MW; 54EF26B46D6C064B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LSVKFG--VLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGVHDDVDI 76
                                                                                                                         glutamate 5-phosphate.
--- PATHWAY: Arginine biosynthesis; second step.
--- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
--- SIMILARITY: BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score ov,
34.0%; Pred. No. 11;
+ive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                 Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001048; Aa kinase.
InterPro; IPR004662; AcgluKinase.
Pfam; PF00696; aakinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=95027704; PubMed=7941342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001118; BAB12772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00761; argB; 1
Arginine biosynthesis; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U77 OR HDRF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELI_HSV6U
P52356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
HELL_HSV6U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylglutamate Kinase (EC 2.7.2.8) (NAG Kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase).
                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S9 KLHKWTQKKENGKKLSKMKVLLKHLTLANLLETLIVMPLDGMWNITVQWYAGELL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 EIHRLGSKNADGKLSVKFGVLFQDDRCANLFEAL-VGTLKAAKRKIVTYAGELL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
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14.9%; Score 60.5; DB 1; Length 328;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 20; Conservative 6; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00001; /tm_+; ...

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

38

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 13;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF018072; AAC27099.2; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
84
                                                                                                                                                                                   MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 1
328 AA;
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
209
272
293
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P57157;
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TRANSMEM
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32792; AAC22774.1; -.
                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus (Horse).
        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9796;
                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YAGELL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAGETL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRHR_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
GRHR_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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      à
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                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVEH-EVNLL------VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AUTO-) (MAJOR SITE).
                                                                                                                                                                                                                                                                               -: - CATALYTIC ACTIVITY: AFP + a protein = ADP + a phosphoprotein. -: - PTM: Autophosphorylated. -: - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                               SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
MEDLINE-97256766; PubMed-9099695;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
                                                                                                                                                                                                               Aebersold R., Pelech S.L.;
"Identification of the autophosphorylation sites of the Xenopus
laevis Pim-1 proto-oncogene-encoded protein kinase.";
J. Biol. Chem. 272:10514-10521(1997).
                                                                                                                                                                                                                                                                                                                               PIM SUBFAMILY.
CAUTION: Was originally (Ref.1) called Pim-1 but seems to represent the pim-3 isoform.
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 61; DB 1; Length 323; 32.6%; Pred. No. 11; tive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (1)
PHOSPHORYLATION (AUTO-).
AB4DD61E7A99A38F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
01sgoeptide transport ATP-binding protein oppf.
0PPF OR HI1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD000001; Euk_pkinase; 1.
PROSTIE; PS00107; PROFIN.KINASE_ATP; F.
PROSTIE; PS00108; PROTEIN.KINASE_ST; 1.
PROSITE; PS50011; PROFEIN.KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                 laevis (African clawed frog)
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71 VAKER--VTEWG--TLNGVMVPLEIVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36964 MW;
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205
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54
69
168
                                                                                                             Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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205
323 AA;
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nes 29; Conserv
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                                                 PIM3 OR PIM1
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P45051;
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MOD_RES
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE-95350630; PubMed=7542800; Patch State St
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSPORT SYSTEM (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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Pred. No. 11;
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Peptide transport; Transport; Inner membrane; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Indels
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45B6A3085431E3D9 CRC64;
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Gonadotropin-releasing hormone receptor (GNRH-R).
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InterPro: IPR003439; ABC_transportr.
Pfam: PF00005; ABC_tran; 1.
ProDom: PD000006; ABC_transportr; 1.
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RESULT 11 OPPF\_HAEIN

SEPTPE

Matches

g ò 9

SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane. PTM: AN INTRAMOLECULAR PHOSPHOTRANSFER TAKES PLACES BETWEEN HIS-554 AND CYS-384.

SUBUNIT: HOMODIMER

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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
PTS system, mannitol-specific IIABC component (EIIABC-MTL) (Mannitol-permease IIABC component) (Phosphotransferase enzyme II, ABC component) (EC 2.7.1.69) (EII-MTL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
MGD618-9431650; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of the mannitol (mtl) operon in Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "S-phosphocysteine and phosphohistidine are intermediates in phosphoenolpyruvate-dependent mannitol transport catalyzed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system. III. The nuclectide sequence of the permease gene.";
J. Biol. Chem. 258:10761-10767(1983).
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116 NTTAEDIFQLGVKQSEGKLLVVFGPLGTD 144
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83291014; PubMed-6309813;
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MEDLINE=88288055; PubMed=3135464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiol. 2:405-412(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3iochemistry 27:5835-5839(1988).
                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 619-637 FROM N.A.
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                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
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                                                                                   RESULT 9
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ģ Sugiyama J.E., Mahmoodian S., Jacobson G.R.; "Membrane topology analysis of Escherichia coli mannitol permease using a nested-deletion method to create mtla-phoa fusions."; Proc. Natl. Acad. Sci. U.S.A. 88:9603-9607(1991). X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 490-637 MEDLINE=98212922; PubMed=9551558; MEDLINE-92052139; PubMed-1946374; POPOLOGY 

MEDILIA DOSALA, FULL.

Van Montfort R.L.M., Priping T., Kalk K.H., Hangyi I.,

Kowwijzer M.L.C.E., Robillard G.T., Dijkstra B.W.;

"The structure of the Escherichia coli phosphotransferase IlAmannitol
reveals a novel fold with two conformations of the active site.";

Structure 6:377-388(1998)

-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBERANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO

CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar - protein histidine + sugar phosphate. SUGAR

323 AA.

PRT;

PIM3\_XENLA STANDARD; 091822; 15-DEC-1998 (Rel. 37, Created)

DA PE

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                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Inner membrane; Phosphorylation; 3D-structure;
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CYTOPLASMIC (POTENTIAL)
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                                             -!- SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.
-!- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS 1 PTS EIIC DOMAIN.
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InterPro; IPR004718; PTSIIC_mtlA.
InterPro; IPR002478; PTS_EIIA_2.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00359; PTS_EIIC.
Pfam; PF02378; PTS_EIIC; 1.
ProDom; PD001689; PTS_EIIC; 1.
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EMBL; X06794; CAA29953.1;
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PDB; 1A3A; 12-AUG-98
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637 AA;
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PIM3_XENLA
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RANSMEM
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                                         A maintenance in yeast requires a protein containing to the GTP-binding domain of dynamin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-53296170; PubMed-8516295;
Lalo D., Carles C., Sentenac A., Thurlaux P.;
"Interactions between three common subunits of yeast RNA polymerases
                                                                                                                                                                                                                                                                                                                               Galisson F., Dujon B.; "Sequence and analysis of a 33 kb fragment from the right arm of ctromosome XV of the yeast Saccharomyces cerevisiae."; Yeast 12:877-885(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 62.5; DB 1; Length 902; 25.6%; Pred. No. 23; Live 18; Mismatches 28; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 90:5524-5528(1993).
-1- FUNCTION: REQUIRED FOR MITTOCHONDRIAL GENOME MAINTENANCE.
-1- SUBCELLUIAR LOCATION: Mitcchondrial.
-1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transit peptide; Mitochondrion.
                                                                                                                   SEQUENCE OF 60-902 FROM N.A.
MEDLINE-93365024; PubMed=7916673;
Guan K., Farh L., Marshall T., Deschenes R.J.;
"Normal mitochondrial structure and genome maintenance in requires the dynamin-like product of the MGMI gene.";
Curr. Genet. 24:141-148(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 ASP-RICH (ACIDIC).
245 GTP (POTENTIAL).
342 GTP (POTENTIAL).
409 GTP (POTENTIAL).
150 G -> C (IN REF. 1 AND 2).
101523 MW; 89BBC745182AA5E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (POTENTIAL). MGM1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07419; -; NOT_ANNOTATED_CDS.
75119; CAA99426.1; -.
                                                                                                                                                                                                                                                                                        STRAIN-S288c / FY1679;
MEDLINE-9643797; PubMed-8840505;
MEDLINE-92192451; PubMed-1532158;
                   Jones B.A., Fangman W.L.; Mitochondrial DNA maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001401; Dynamin.
Pfam; PF00350; dynamin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 179-902 FROM N.A.
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Motor protein; GTP-binding; T
TRANSIT 7 902
CHAIN
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                                                                                                                                                                                                                                                                    SEQUENCE OF 1-805 FROM N.A.
                                                                                Genes Dev. 6:380-389(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYNAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00195; DYNAMIN
SMART; SM00053; DYNC; 1.
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PIR; S19068; S19068.
SGD; S0005737; MGM1.
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238
338
406
150
                                                              a region related
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NP_BIND
NP_BIND
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RRYRY RYRY RRYRY R
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Gaps

21;

28; Indels

23; Conservative

Matches

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Local Similarity

EHEVNLLVEEIHRLGS-----KNADG--KLSVKFGVLFQDDRCANLFEALVGTLKAA---

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Alexandre 5., Paindavione P., Tebabi P., Pays A., Halleux S., Steinert M., Pays E.; Tebabi P., Pays A., Halleux S., Steinert M., Pays E.; Tebabi P., Patificential expression of a family of putative adenylate/guanylate cyclase genes in Trypanosoma brucei.";
Mol. Biochem. Parasitol. 43:279-288(1990).
-!- FUNCTION: COULD ACT AS A RECEPTOR FOR A UNKNOWN LIGAND.
-!- FUNCTION: MEMP = 3',5'-cyclic AMP + diphosphate.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Receptor-type ademylate cyclase GRESAG 4.1 (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1242;
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N-LINKED (GLCNAC...) (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Receptor; Glyco CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                   PRT; 1242 AA
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS50125; GGANYLATE_CYCLASES_2; 1.
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Pred. No. 3
                                                                                    ------KRRKIVTYAGELLLQGVHDDVD 75
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                                                                                                                          774 GSEAIFLDKRCKVLSFRLKMLKNKCHSTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei brucei
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; cAMP synthesis;
DOMAIN 1 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=EATRO 1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRESAG 4.1.
                                                                                                                                                                                                                                                                                CY41_TRYBB
Q99279;
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                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96127529; Pubmed-8590279;
MEDLINE-96127529; Pubmed-8590279;
Sugiana M., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiana M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 k region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO B.SUBILLS YOFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 63; DB 1; Length 811; 22.1%; Pred. No. 18;
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18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL F6015BEBF804F255 CRC64;
                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces
      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGMI_YEAST STANDARD; PRT; 902 AA. P32266; Q08627; Q02609; 01-00T-1997 (Rel. 27, Casted) 10-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
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MGM1 OR YOR211C OR YOR50-1.
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InterPro; IPR003607; ME_Pplase_HDc.
Pfam; PF01966; HD; 1.
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TIGREAMS; TIGRO0277; HDIG; 1.
Hypothetical protein; Transmer
                                                             Hypothetical protein slr0104.
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SEQUENCE OF 60-902 FROM N.A.
STRAIN-BJ41-8C;
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Matches 15; Conservative
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                                                                                                                                             NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                       - Prospundances-cert.
- Prospundances-coardon: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.6%; Score 63.5; DB 1; Length 231; Best Local Similarity 27.1%; Pred. No. 3.9; Matches 23; Conservative 15; Mismatches 30; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 EHEVNLLVEEIHRLGSKNAD-GKLSVKFGVLFQDDRCANLFEAL------VGTLKA 52
                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7355F5A8039A4747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Nuclease; Endonuclease; RNA-binding.
DOMAIN 3 131 RNASE III.
                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                         231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         811 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: || | | | | 108 ARLRKSVLGDICEAVIGAIFLDGGH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AKRRKIV-----TYAGELLLQGVH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART, SM00358; DSRM; 1.
SMART; SM00358; RIBGC; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50157; RRANSE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF065159; AAD02939.1; -. InterPro; IPR001159; DS_RBD. InterPro; IPR000999; RNase_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 D
25071 MW;
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphomonoester
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-USDA 110spc4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 AA;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=375;
:|||
124 WNDVD 128
                                                                                                                                                                            30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y104_SYNY3
ID Y104_SYNY3
AC P54371;
                                                                                                                  RNC_BRAJA
069161;
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RESULT 6

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Pfam; PF00047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV2I_HUMAN
P06331;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV2I_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                        [1]
SEQUENCE FROM N.A.
SERINB-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-56337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb L.M., Clayton R.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts R.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 IEHKVRDAFLLSEMLNAVG---RNGLFAVGIGICLEDDECIKIGNQILWEYKKNLINELK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VEHEVN----LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANL-----FEALVGTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87031575; PubMed-3095189;
Paces V., Vlcek C., Urbanek P., Hostomsky Z.;
"Nucleotide sequence of the right early region of Bacillus subtilis
phage PZA completes the 19366-bp sequence of PZA genome. Comparison
with the homologous sequence of phage phi 29.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
phi-29-like viruses.
NCBI_TaxID=10757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 44:115-120(1986).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPLICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.0%; Score 65; DB 1; Length 432; 26.9%; Pred. No. 5.3; ive 15; Mismatches 20; Indels
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .l protein; Complete proteome.
432 AA; 48835 MW; 0EB95D188D2B41F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Early protein GP17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 AA.

    -1- SIMILARITY: TO M.JANNASCHII MJ0977.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003156; DHHA1.
InterPro; IPR001167; Ppesterase.
Pfam; PP01368; DHH; 1.
Pfam; PF02272; DHHA1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        jannaschii.";
Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67526; AAB98830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage PZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | :|:
326 SVKLKKL 332
                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AAKRRI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VG17_BPP2A
P08389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
VG17_BPP2A
VG17_BPP2A
C P08389;
DT 01-AUG-
DT 15-DEC-
DT 15-DEC-
DT 17. VG
C VITUSEC
C 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  QC
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LLEVTVEELGEQONDDDLDEIDSELYEDAEASDVPHETIVKVFEADK--SIVTFNGEKLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 IGEINHSGSTNY--KTSLKSRVTISLDTSKNLFSLKLSSVTAAD--TAVYYCARGLLRGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-85205331: pubMed-3922855;
Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";
Gene 33:181-189(1985).
PIK: A02101; G1HUH2.
HSSP: P01825; 7FAB.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANL-FEALVGTLKAAKRKIVTYAGELLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     э;
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V-II REGION ARH-77.
                                                                                                                                                                                                                                                                                                                                                                     Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Indels
SIMILARITY: BELONGS TO THE PODOVIRUSES GP17 FAMILY.
                                                                                                                                                                                                                                                                                         Early protein; DNA replication.
SEQUENCE 174 AA; 20022 MW; 08FBC8F91D4B4224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB 1;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 06, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V-II region ARH-77 precursor. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 64.5; Di
32.4%; Pred. No. 2.2;
ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                           EMBL; M11813; AAA88499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarion
hes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ig; 1.
6; IGv; 1.
                                                                                                                                                                                                                                                                    PIR; F29004; WRBP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |||
120 HYVNVDVD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 QGVHDDVD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00406;
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coturnix co
thermotoga
human herpe
bacillus su
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                                                                                                   January 17, 2003, 01:34:28; Search time 78 Seconds (without alignments) 43.072 Million cell updates/sec
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1 MNVEHEVNLLVEEIHRLGSK......AGELLLQGVHDDVDIVLLQD 81
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Q9urv2
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                   112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y831_METJA
WGT_BPPZA
HYZ1_HUMAN
RNC_BRAJA
Y 104_SYNY3
MGML_YEAST
CY41_TRYBB
PTMA_ECOLI
PTMA_ECOLI
OPPE_HAETN
GRHR_HORSE
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ASTL_COTJA
FTSZ_THEMA
HELI_HSV6Z
RL27_BACSU
PME_PRUPE
PL10_MOUSE
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DDX3_MOUSE
CAPP_RHOPA
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YN8V_YEAST
ASB2_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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YJDA_ECOLI
                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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ST P10507 saccharomyc PA 042821 candida par 042821 candida par P00474 providencia Q9K723 bacillus ha 066218 pantoea ana 09anr8 sodalis glo P42173 caenorhabdi P24240 escherichia P24240 escherichia P24240 escherichia Q9x597 bacillus th P3 Q9x597 bacillus th P3 Q9x897 bacillus the P3 Q9x897 bacill	MENTS	1403 AA.	n update)	il catfish virus) (CCV). stage; Herpesviridae;	of herpesvirus.";	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):	FA6E366FC04A33AE CRC64;	re 66; DB 1; Length 1403; d. No. 15; Mismatches 30; Indels 20; Gaps 3;	VEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGT 49 		432 AA. update) n update)
MPPB_YEAST GAL1_CANPA MTPS_PROST ARAG_PACHD CH60_PANAN CH60_SODGL YKL6_CABEL CQAA_BACTF ASCB_ECOLI FLHA_HELPJ SHK3_RAT	ALIGNMENT	PRT; ed)		ë a ·	727613; new type o	pyright. of Biol Institut utions as is not r agreemen	MW; FA6	Sco Pre 7;	KLSVKFGVL : LRKLNNAYL	r 66 * 860	PRT; 432 AA. ed) sequence update) annotation updat
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462 504 507 517 541 922 1163 474 474 1813 354		1NDAR 24, 24,	24, L	irus l ruses, like v	FROM N.A. uburn 1; 92087490; PubMec A.J.; catfish virus: 186:9-14(1992).	ntry is Inst. nformatit in state	AAA88125.1; E36788. protein.	vat	HRLGSKI   1  ART-KK	LKAAKRRKIVTYAGELL     :  :  :  :  :  LDEANKRITTLTQRLATVSGELV	STANDARD; Rel. 35, Creat Rel. 35, Last Rel. 40, Last protein MJ0831
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		JT 1 HSVI1 VG22_HSVI1 Q00105; 01-DEC-1992	01-DEC-1992 Hypothetical 22.	Ictalurid herpesvirus 1 Viruses; dsDNA viruses, Ictalurid Herpes-11ke vi NCBI_TaxID=10401;	SECULORICE FROM N.A. STRAIN-Auburn 1; MEDLINE-92087490; PubMed-1727613 Dayison A.J.; "Channel catfish virus: a new tyl Virology 186:9-14(1992).	is SWISS ttween te Europe to by totities send an	EMBL; M75136; PIR; E36788; Hypothetical SEQUENCE 140	itch	3 VEHEY     779 VEVR	38	LT 2 METJA 058241; 01-NOV-1997 01-NOV-1997 16-OCT-2001 Hypothetical MJ0831.
88888844444 48867880012848		RESULT 1 VG22_HSV11 ID VG22_ AC Q0010 DT 01-DE	01 22	2425	SE SE C	or a character is	PI	Query Ma Best Loc Matches		60	RESULT 2 Y831_METJA AC 05824 DT 01-NO DT 16-OC DE HYPOU
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A;Residues: 1-2535 <BEV>
A;Cross-references: EMBL:AL035440
A;Cross-references: EMBL:AL035440
C;Genetics: cultivar Columbia; BAC clone F10M23
C;Genetics: A;Map position: 4
A;Introns: 395/1; 613/3; 777/1; 826/3; 1945/2; 1993/3; 2061/3; 2129/3; 2178/3; 2295/3; A;Note: F10M23.350
                                                                                                                                                                                                                                                                                                                           Query Match 15.5%; Score 63; DB 2; Length 2535; Best Local Similarity 30.0%; Pred. No. 2.4e+02; Matches 27; Conservative 13; Mismatches 32; Indels 18; Gaps
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Search completed: January 17, 2003, 02:17:36 Job time : 52 secs

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A; Map position: X
A;Introns: 87/3; 106/2; 151/3; 186/2; 210/3; 237/3; 268/3; 291/2; 334/1; 363/2; 404/3
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10634.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T04824
R; Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes submitted to the Protein Sequence Database, February 1999
A; Reference number: 215385
A; Accession: T04824
                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 HEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK----AAKRRKIVT 60
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                                                                                                                                                                                                                                                                                                                                               GSPDB:GN00028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; DB 2; Length 514;
Pred. No. 39;
4; Mismatches 13; Indels
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                                              homolog - Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. (strain PCC 6803)
                                                                                                                                                             submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid M02A10.
                                                                                                                                                                                                                                                                                                           A; Residues: 1-514 <MIN>
A; Cross-references: EMBL:U58730; PIDN:AAC48058.1; GSPDE
A; Experimental source: strain Bristol N2; clone M02A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76690
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                                                                                                                                                                                                                                        A, Accession: T29652
A, Status: preliminary, translated from GB/EMBL/DDBJ
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18; Mismatches
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Pred. No.
                                         inward rectifier potassium channel
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ilarity 49.1%;
Conservative
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22.1%;
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Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
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hypothetical protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-811 <KAN>
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                                                                                                                                                                                                                                                                                       A; Molecule type: DNP
                                                                                                               C; Accession: T29652
R; Minx, P.; Le, T.T
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                                                                                                                                                                                                                                                               Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A:Accession: H72336
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-599 < ARN>
A:Cross-references: GB:AE001746; GB:AE000512; NID:g4981285; PIDN:AAD35852.1; PID:g498129
C:Genetics:
A:Genetics:
A:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P84784

P070bable glucosyl transferase [imported] - Arabidopsis thaliana

P070bable glucosyl transferase [imported] - Arabidopsis thaliana

P070bable glucosyl transferase [mouse-ear cress)

C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: F84784

R.Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Roo, H.; Moffat, R.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                     Hickey
                                                                                                               conserved hypothetical protein - Thermotoga maritima (strain MSBB)
(Species: Thermotoga maritima
(Species: Thermotoga maritima
(Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
(SAccession: H72336
(SAccession: H72336
(SAccession: K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicker Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 2; Length 599;
Pred. No. 36;
9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 63.5; D
; Pred. No. 33;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Map position: 2
Superfamily: flavonol 03-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 ARISYHDPRMSLLEGVFSRGDRKLL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 KIVTYAGE--LLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 VEKGGSSHSNITL-LLQD 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 V-----HDDVDIVLLQD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 15.8 Best Local Similarity 36.5 Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-496 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: F84784
A; Status: preliminary
124 WNDVD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g36780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
Matches 25;
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A; Molecule type: DNA

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C;Species: phage PzA A;Note: host Bacillus subtilis C;Species: phage PzA A;Note: host Bacillus subtilis C;Date: 31-Mar-1988 #text_change 23-Jul-1999 C;Accession: F29004 C;Accession: F290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Homo sapiens (man)
C.bate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C.bate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C.Accession: A03101.
R.Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 188
A; Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat se
A; Reference number: A02101; MUID:85205332; PMID:3922855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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C.Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LLEVTVEELGEQDNDDDLDEIDSELYEDAEASDVPHETIVKVFEADK--SIVTFNGEKLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 IGEINHSGSTNY--KTSLKSRVTISLDTSKNLFSLKLSSVTAAD--TAVYYCARGLLRGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANL-FEALVGTLKAAKRRKIVTYAGELLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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as Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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for residue 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain precursor V-II region (ARH-77) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     四 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 15.9%; Score 64.5; Di Local Similarity 32.4%; Pred. No. 7.9; nes 22; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:35-117/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Residues: 1-146 < KUD>
A; Residues: 1-146 < KUD>
A; Note: the sequence was determined from the A; Note: the authors translated the codon GGG C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: GDB:128528; OMIM:147070
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F;128-146/Region: J segment
F;42-115/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 14q32.33-14q32.33
A; Introns: 16/3
early protein gp17 - phage PZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F; 20-117/Region: V segmen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0977
                                                                                                                                                                                                    Cyaccession: E36788
Rybavison, A.J.
submitted to Genenk, January 1992
A) Description: Channel catfish virus: a new type of herpesvirus.
A) Reference number: A36804
A) Accession: E36788
A) Accession:
                       hypothetical protein ORF22 - ictalurid herpesvirus 1 (strain auburn 1)
C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: E36788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Methanococcus jannaschii
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      780 VEVRVNLLTEELART-KKTVDELRKLNNAYLTAKDRLQARVEALTTDNQSMKLLVGNGGT 838
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19;
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Pred. No. 56;
7; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
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Pred. No.
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illarity 26.9%;
Conservative 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.3%;
ilarity 31.3%;
Conservative
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | :|:
SVKLKKL 332
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A;Residues: 1-395 <PAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72997.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F28A21.200 - Arabidopsis thaliana (C.$pecies: Arabidopsis thaliana (mouse-ear cress) (C.$pecies: Arabidopsis thaliana (mouse-ear cress) (C.bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Sep-1999 (C.Accession: T04871 M.W. Mueller, M.W. Mueller, M.W. Mueller, M.W. Mueller, M.W.; Mueller, M.W.; Mueller, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                          R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
Nature 403, 665-668, 2000
A;Itile: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: F81343
                                                                                                                                                                                                                                                      probable integral membrane zinc-metalloproteinase Cj0723c [imported] - Campylobacter
                                                                                                                                                                                                                                                                                   C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 VSFMINLFVTAVFAKGFYGTKQADSIGLVNAGYYLQEKYGGGVFPILYIWGIGLLAAGQS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NVEHEVNLLVEE-----IHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VEHEVNLLVEEIHR---LGSKNADGKLSVKFGVLFQDDRCANLFEAL----VGTLKAAKR 55
44 EVSLLVE-----SKSDVKDGFNFVVLDQDQKQYESFCQDLFESRKGKDSLESVQKALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 193/2; 239/1; 456/3
A;Note: F28A21.200
C;Superfamily: natural resistance-associated macrophage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68.5; DB 2;
Pred. No. 7.1;
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red. No. 19;
Mismatches 36
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26.2%; Pred. No. /...
've 19; Mismatches
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Similarity 29.5%; Pred. No.
23; Conservative 11; Mismatc
                                                                                                                      TRPF--YAMMLLKKGFFDGV 114
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                                                                         55 RRKIVTYAGELLLQGVHDDV 74
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Best Local Similarity 26.2%
Matches 21; Conservative
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A; Residues: 1-530 <BEV>
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                                                                                                                                                                                                                                                                                                                                    C; Accession: F81343
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Best Local Sim:
Matches 23;
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Nucleic Acids Res. 29, 2145-2153, 2001
A;fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MYPU_2370 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C.Species: Mycoplasma pulmonis C;Species: Ay.May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: E99541
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A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:235663; PIDN:CAA84722.1; GSPDB:GN00021; CESP:T04A8.4
A;Experimental source: clone T04A8
                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T04A8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24421
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: 219889
A:Accession: T24421
A:Status: preliminary: translated from GB/EMBL/DDBJ
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                                                                                                              2 NVEHEVNLLVEEIHRLGSKNADG-KLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
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                                                                         <u>ښ</u>
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                  Length 162;
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          23.8%; Score 96.5; DB 2; Length 1 32.9%; Pred. No. 0.002; ive 16; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 3
A; Introns: 26/2; 58/3; 102/3; 191/2; 223/3
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C;Superfamily: phosphate acetyltransferase
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111 RKYGLVHFEGEMLYQRQDDEXIITML 136
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                                     Similarity 32.9:
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A;Molecule type: DNA
A;Residues: 1-318 <KUR>
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                Query Match
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Matches 2
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Gaps

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Indels

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Length 395;

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Length 530;

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January 17, 2003, 02:02:38 ; Search time 49 Seconds (without alignments) 158.916 Million cell updates/sec
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406
1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD 81
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                           OM protein - protein search, using sw model
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Perfect score:
Sequence:
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283224 segs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	TOTAL TOTAL	hypothetical prote				O)	hypothetical prote			c	Iq heavy chain pre	conserved hypothet	probable qlucosyl	inward rectifier p	hypothetical prote	hypothetical prote	probable qlucosyl	probable glucosyl	methyl-accepting c	dynamin-like prote	hypothetical prote	probable adenylate	phosphotransferase	glutamate-ammonia-	hypothetical prote	potential acras op	oligopeptide trans	probable adhesin N	hypothetical prote	methyl-accepting c .
ID		T04981	T21860	T24421	E90541	F81343	T04871	E36788	G64403	WRBP70	G1HUH2	H72336	F84784	T29652	876690	T04824	C84784	D84784	G64532	S33918	AE2515	S14201	WOEC2M	AE2697	E97479	AH0561	B64184	A81931	T15904	F71975
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Query Match Length		161	162	289	318	395	530	1404	432	174	146	599	496	514	811	2535	491	496	565	902	268	1242	637	988	1010	217	332	256	635	564
Query		70.4	23.8	20.1	17.0	16.9	16.3	16.3	16.0	15.9	15.8	15.8	15.6	15.5	15.5	15.5	15.4	15.4	15.4	15.4	15.3	15.3	15.1	15.1	15.1	15.0	15.0	15.0	15.0	14.9
Score		386	96.5	81.5	69	68.5	99	99	65	64.5	64	64	63.5	63	63	63	62.5	62.5	62.5	62.5	62	62	61.5	61.5	61.5	61	19	61	61	60.5
sult No.		1	7	٣	4	ഗ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	74	52	56	27	28	53

RESULT 2

r21860

hypothetical protein F36F2.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C; Accession: T21860
R; Cottage, A.
submitted to the EMBL Data Library, November 1996
A; Accession: T21860
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; McGeoule type: DNA
A; McGeoule t

C;Genetics: A;Gene: CESP:F36F2.1 A;Map position: 1 A;Introns: 9/1; 28/1; 64/1; 108/3

hypothetical prote	acetyigiutamate Ki 3-hydroxyacyl-CoA methionyl-tRNA syn	helicase [imported calmodulin - yeast	metalloproteinase cell division prot	U4/U6-associated R U4/U6 small nuclea	hypothetical prote hypothetical prote	galactoside transp hypothetical prote	hypothetical prote
F96560 D88486	D84335 D84286 D82249	T44037 MCBY	S41055 H72328	T50840 T50839	E69425 G64504	AH0183 C91188	C86035
000	9 79 79	77	0 0	0 0	77	01 01	7
573 1870	659 731	824 147	310 351	682 683	775 287	506 637	637
14.9	14.8 14.8	14.8 14.7	14.7	14.7	14.7 14.5	14.5	14.5
60.5	999	60 59.5	59.5 59.5	59.5 59.5	59.5 59	50 20	29
30	333	35 36	37 38	39 40	4 4 7 7	<b>4</b> 4	45

## ALIGNMENTS

RESULT 1  hypothetical protein T1611.130 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 24.Nov-1999 C:Caccession: T04981 C:Date: 21.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 24.Nov-1999 C:Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 24.Nov-1999 C:Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 24.Nov-1999 C:Date: 23.Apr.1999 #sequence_revision 24.Nov-1999 C:Date: 23.Apr.1999 #sequence_revision 24.Nov-1999 C:Date: 23.Apr.1999 #sequence_revision 24.Nov-1999 C:Date: 21.Date: 21.Date: 21.Nov-1999 C:Date: 21.Date: 21.Date: 21.Nov-1999 C:Date: 21.Date: 21
tchan 11, E.; 198 T16L T16L indels LIVGTLK LLVGTLK

Search completed: January 17, 2003, 02:18:24 Job time : 37 secs

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SEQ ID NO 91
LENGTH: 660
TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                      Query Match 13.4%; Score 54.5; DB 4; Length 128; Best Local Similarity 30.6%; Pred. No. 8.7; Matches 26; Conservative 13; Mismatches 35; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 4 EHEVNLLVEEIHRLGS-----KNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NVEHEVNL----LVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
APPLICANT: Page, David
APLICANT: Page, Solve
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WH197-08pA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 91, Application US/09058489
Patent No. 6103886
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehead institute for Biomedical Research
APPLICANT: Whitehead institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 54.5; DB 3; Length 660; 27.1%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 SEQ ID NO 4164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PastSEQ for Windows Version 3.0
EED ID NO 18
LENGTH: 660
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CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 KNVESFINLLNOMVKSNVEKALROD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 KIVTYAGELLLQGVHDDVDIVLLQD 81
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10S-09-058-489-18
Sequence 18, Application US/09058489
Patent No. 6103886
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Best Local Similarity
Matches 16; Conserv
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US-09-058-489-18
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US-09-058-489-91
                                                                                                                                                                                     LENGTH: 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3066;
                                                                                                                                                                                          Length 660;
                                                                                                                                                                                      13.4%; Score 54.5; DB 3; Length 6
27.1%; Pred. No. 69;
tive 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 NLLVEEIHRLGSK----NADGKLSVKFGVL-FQDDRCANLFEALVGTLKAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: SOOD NO. 6211336thwestern Hwy., Suite 410 CITY: Farmington Hills STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tagle, Danllo A.
APPLICANT: Tagle, Danllo A.
APPLICANT: Tagle, Danllo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rohn & Associates
STREET: 30500 No. 6211336thwestern u...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 54.5; DB 4;
; Pred. No. 4.7e+02;
16; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KRRKIVTYAGELL---LQGVHDDVDIV 77
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/08952127
; Patent No. 6211336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5050
TELEPHONE: 810-539-5055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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26.6%;
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                                                                                                                                                                                                                                16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 48334
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shiloh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Gaps

us-09-648-310-2.rai

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; Sequence 4164, Application US/09134001C; Sequence 4164, Application US/09134001C; Patent No. 6380370; Patent No. 6380370; APPLICANT: Lynn Doucette-Stamm et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC; TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VLLTVEENDSQKPQNADSKLPEDQLTPGDGHHVNRVFRPGLSDSTSAKSQVLFETEVSRK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SVKFGVLFQDDRCAN 41
                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                            Length 2206;
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                                                                                                                                       30; Indels
                                                                                8; Indels
                                                                                                                   ----RRKIVTYA---GELLLQGVHDDVDIV 77
                                                                                                                                                                                                                                                Sequence 14, Application US/08203905B
Patent No. 5646549
GENERAL INFORMATION:
APPLICANT: KAYE, FEDERIC J.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF ITLE OF INVENTION: NOVEL CHAPERONE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            5: KNOBBE, MARTENS, OLSON & BEAR
620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/203,905B
FILING DATE: February 28, 1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 LF----NTLNEDLFQKILVPIQQVLKEGLLDKTEIDEVVL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 LFEALVGTLKAAKRRIVTYAGELLLQGVHD--DVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                            DB 4;
                                        13.8%; Score 56; DB 4; 36.2%; Pred. No. 2e+02; ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KIRKFATRICK, ANITA M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH089.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.78; 27.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 472 amino acids TYPE: amino acid
                                    Query Match 13.8
Best Local Similarity 36.2
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Conservative
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COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                   47 VGTLKAAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-09-134-001C-4164
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                                                                                                                                                                                                                                US-08-203-905B-14
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US-08-465-250-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 2; Length 2206;
Pred. No. 2e+02;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1553 VPTIRAAKVOGPGFDYAVAMAKRNIVTATTSKGEFTMLGVHDNVAIL 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 VGTLKAAK-----RRKIVTYA---GELLLQGVHDDVDIV 77
                      SOFTWARE: Patentin Release #1.0, Version #1.25 CHREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-JUN-1995
                                                                                                                                                                                   36607-D-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/465,250 FILING DATE: 6-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release 1.30
                                                                                                                                   NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 3660;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08465250 Patent No. 6136570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%;
36.2%;
                                                                                                                     ATTORNEY/AGENT INFORMATION:
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TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 2206 amino acids amino acid
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Best Local Similarity 36.2
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-461-503-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                              FILING DATE: 5-CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Racani
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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ZIP: 10036
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US-07-852-260-2
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                14 IHRLGSKNADGKLSVKFGV----LFQDDRCANLFEALVGTLKAAKRRIVTYAGELLLQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 IHRLGSKNADGKLSVKFGV----LFQDDRCANLFEALVGTLKAAKRKIVTYAGELLLQ 68
                                                                                                                                                             Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-619-062-2

Sequence 2, Application US/09619062

Patent No. 6406875

GENERAL INFORMATION:

APPLICANT: Shisheva, Assia

TITLE OF INVENTION: No. 6406875el Mammalian Putative

TITLE OF INVENTION: Phosphatidylinositol-4-Phosphate-5-Kinase

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                                        Length 2052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/619,062
                                                                                                                                                             23;
                                                                                                                    ; Score 56; DB 3;
; Pred. No. 1.8e+02;
15; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828
CITY: Bloomfaeld Hills
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F
REFERENCE/DOCKET NUMBER: 4981-098431
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,201
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPANE: (248) 641-1600
TELEFAX: (248) 641-0270
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
.LENGTH: 2052 amino acids
                                                                                                                    Ouery Match 13.8%;
Best Local Similarity 26.0%;
Matches 19; Conservative 19
LENGTH: 2052 amino acids
                    TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: unknown unknown
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1922 ---ESCDWLLDE 1931
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1922 ---ESCDVVLLDE 1931
                                                                                                                                                                                                                                                                                 69 GVHDDVDIVLLQD 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: un]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                              ; TOPOLOGY:
US-09-045-201A-2
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Gaps
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                                                         APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08461503
Patent No. 5834302
GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: RETHODS FOR PRODUCING RNA VIRUSES
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILING DATE: 19920619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1;
Pred. No. 2e+02;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19920619
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENG-JOCKET NUMBER: 36607-B-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 2, Application US/07852260 Patent No. 5525715 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.8%
Best Local Similarity 36.2%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-852-260-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 VGTLKAAK-----
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Query Match

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                                                                                      Sequence 15, Application US/09058489
Fatent No. 6103886
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
SERVIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                              2 NVEH-EVNLL------VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09058489
Fatent No. 6103886
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTIONS: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
WUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NVEHEVNL----LVBEIHRLGSKNADGKLSVKFGVLFQDDRCANLFBALVGTLKAAKR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.4%; Score 58.5; DB 3; Length 662; 28.8%; Pred. No. 20; ive 12; Mismatches 23; Indels
   .; Score 61; DB 4; Length 323;
.; Pred. No. 3.8;
13; Mismatches 27; Indels
                                        27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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; Pred. No. 20;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : FastSEQ for Windows Version 3.0
                                                                                                                                  52 AAKRRKIVTYAGELLLQGVHDDVDIVLLQ 80
                                                                                                                                                          15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; 28.8%;
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Best Local Similarity 28.8%
Matches 17; Conservative
                               29; Conservative
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            Best Local Similarity
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-058-489-16
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US-09-058-489-15
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LENGTH: 662
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LENGTH: 662
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                               Matches
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOG

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-14

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-108-14

SEQ ID NOS: 5674

LENGTH: 208
                          10 LVEEIHRLGSKNADGKLSVKFGVL----FQDDRCANLFEALVGTLKAAKRKIVTYAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NVEHEVNL----LVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Shisheva, Assia
TITLE OF INVENTION: No. 6110718el Mammalian Putative
TITLE OF INVENTION: Phosphatidylinositol-4-Phosphate-5-Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 208;
10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; Score 56; 28.2%; Pred. No.
                                                                                                                                                 Sequence 2873, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/045,201A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09045201A Patent No. 6110718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F
REFERENCE/DOCKET NUMBER: 4:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (248) 641-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| : : :||||
| 80 EILTRHI----TLLLQD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. BOX 828
CITY: Bloomfield Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 46303
ZIP: 46303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compe
OPERATING SYSTEM: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Watches 22; Conserv
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                                                                                                                           US-09-134-001C-2873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-045-201A-2
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US-09-644-450-6
Sequence 6, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVEH-EVNLL------VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 61; DB 4; Length 323; 32.6%; Pred. No. 3.8; tive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AAKRRKIVTYAGELLLQGVHDDVDIVLLQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 32.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Xenopus laevis
US-09-237-543-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Xenopus laevis
US-09-644-450-6
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2, Appli
2, Appli
2, Appli
2, Appli
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14, Appl
4164, Ap
18, Appl
91, Appl
12, Appl
11, Appl
29, Appl
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Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           January 17, 2003, 02:04:14; search time 36 Seconds (without alignments) 66.202 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6,
                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence
Sequence
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Sequence
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1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD
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                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-058-489-15
US-09-058-489-16
US-09-134-001C-2873
US-09-045-201A-2
US-09-619-062-2
US-07-852-260-2
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US-08-465-250-2
US-09-134-0010-4164
US-09-058-489-18
US-09-058-489-11
US-09-058-489-11
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US-09-347-801-16
US-08-914-375C-60
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-981-527A-11
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                                                                                                                                                                                  262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                            seq length: 0 . seq length: 2000000000
                                                                                                         US-09-648-310-2
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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                                                                                                         Title:
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Gaps

20;

27; Indels

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4771, Ap
5619, Ap
2, Appli
2, Appli
                                                                                                                                                                      10, Appl
8, Appli
10, Appl
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22, Appl
4, Appli
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 6
LENGTH: 323
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        Sequence
                                                                      US-08-836-943-2
US-08-095-726-8
US-08-095-726-10
US-08-096-043-10
US-08-096-043-10
US-09-096-623A-10
US-09-291-922-22
US-09-0134-001C-4771
US-09-134-001C-5619
US-09-14-057-2
    US-08-059-032-5
PCT-US91-07290-5
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; Sequence 6, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1158
            GENERAL INFORMATION:
APPLICANT: Kathariou, Sophia
APPLICANT: Lei, Xiang-Heis
TITLE OP INVENTION: Secrotype-Specific Probes for Listeria Monocytogenes
FILE REFERENCE: A65378/RFT/DSS
CURRENT APPLICATION NUMBER: US/09/115,150
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 405 EEEINKLGYEVYQNEYKNATGKDAVSYNEYKR--RIDDSTNPLISISKAPSLKKITDSIY 462
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                                                                                                                                                                                                                                                                                                                         Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1158, Application US/09925301
Patent No. US20020052308a1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPRENCE: Palo6
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: PST/VS00/05882
PRIOR APPLICATION NUMBER: 05010-03-08
PRIOR APPLICATION NUMBER: 067/124,270
                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                           13; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                     Score 54.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09817514A
patent No. US20020078478A1
PERERAL INFORMATION:
APPLICANT: ffrench-Constant, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 A-----GELLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                     13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 1158
LENGTH: 639
                                                                                                                                                                                                                                                                                                                 Query Match 13.4%
Best Local Similarity 29.8%
Matches 25; Conservative
Patent No. US20010055759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                       ; ORGANISM: Bacterial US-09-115-150-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-925-301-1158
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                                                                                                                                                                                                                  LENGTH: 549
TYPE: PRT
                                                                                                                                                                                                 SEQ ID NO 4
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8
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APPLICANT: Escheleau, Thomas
APPLICANT: Waterfield, Nicholas
APPLICANT: Waterfield, Nicholas
TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
FILE REFERENCE: 61645
CURRENT APPLICATION NUMBER: US/09/817,514A
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/191806
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2389 ASVSFADLKIREDYPASLGKIRRIKQISVTLPA----LLGPYQDVQAIL 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nicolaides, Nicholas
APPLICANT: Sass, Philip
APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luigi
APPLICANT: Grasso, Luigi
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: Weast
FILE REFERENCE: 01107.00097
CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                                                                                                                                         Score 54.5; DB 10;
Pred. No. 3.2e+02;
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12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LVEEIHRL
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 17, 2003, 02:19:49 Job time: 73 secs
                                                                                                                                                                                                                                                                                                    ORGANISM: Photorhabdus luminescens US-09-817-514A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09788657 Patent No. US20020123149A1
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23.9%;
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Best Local Similarity 29.2%
Watches 14; Conservative
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Best Local Similarity 23.99
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus US-09-788-657-16
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                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 2516
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LENGTH: 859
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APPLICANT: Smith, Hilda
TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR APPLICATION NUMBER: EP98202465.1
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR FILING DATE: 1998-07-22
SUFFURE FILING DATE: 1998-07-22
SUFFURE: PATENTING DATE: 1998-07-22
SUFFURE: PATENTING DATE: 1998-07-22
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Patent No. US20020094551A1

GENERAL INFORMATION:

APPLICANT: ADLER, JON ELLIOT

TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
FILE REPERENCE: 078003/0279152/RXT

CURRENT APPLICATION NUMBER: US/09/825,882

CURRENT FILING DATE: 2001-04-05

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-11-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver: 2.1
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136 GTVVGLLNIRMVGEASAEGKLELLQKARGHKKSVTAAFEEMKRAGYDGGRIVM 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 VLFQDDRCANLFEALVGTLKAAKRRIVTYAGELL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; D
Pred. No. 22;
8; Mismatches
                                                                                 Sequence 10, Application US/09767041
Patent No. US20020055168A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 13.4%;
l Similarity 42.9%;
l5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 13.4%
Best Local Similarity 24.8%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; OTHER INFORMATION: ORF2Z
US-09-767-041-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-882-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 10
LENGTH: 239
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APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zabrowicz, Brian
TITLE OF INVENTION: No. 0520020038011A1e1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2001-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| |: :| |:|
-----LHRDIKSQNIFLTRD 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1160;
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13.5%; Score 55; DB 10;
Best Local Similarity 28.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 12; Mismatches 17
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FLILING DATE: 2000-03-21
PRIOR FLILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-22-22
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13.7%; Score 55.5; D
Best Local Similarity 24.2%; Pred. No. 89;
Matches 16; Conservative 14; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020038011A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10047
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; ORGANISM: homo sapiens
US-09-783-320-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 LGEYFL 278
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RESULT 12 US-09-115-150-4 ; Sequence 4, Application US/09115150

RESULT 10

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32 VNLKVRPHSIHALMGENGAGKSTLLKCLFGI-YQKDSGTILFQGKEIDFHSAK----- 83
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                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokarvotes
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Pred. No. 27;
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       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PELING DATE: 2001-12-22
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                                                                                                                                               Sequence 10214, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                      Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
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ilarity 32.5%;
Conservative
                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14110
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US-09-815-242-10214
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Galina, Chestukhina
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
CURENT APPLICATION NUMBER: US/09/756,526A
CURRENT FILING DATE: 2001-01-08
PRIOR PPLICATION NUMBER: US 60/175,158
PRIOR PPLICATION DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
LENGTH: 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 57; DB 10; Length 1163; ilarity 35.1%; Pred. No. 58; Conservative 11; Mismatches 22; Indels .
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TILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRICE APPLICATION NUMBER: 60/191,078
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Mismatches
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NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10270
SEQ ID NO 10270
LENCTH: 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
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REPLING DATE: 2000-03-21
RETLING DATE: 2000-05-23
REPLING DATE: 2000-05-23
REPLING DATE: 2000-05-26
REPLICATION NUMBER: 60/242,578
REPLICATION NUMBER: 60/242,578
REPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus thuringiensis
US-09-756-526A-2
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Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
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Carr, Grant J.
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nes 20; Conserv
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Length 506;

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7 VNLLV--EEIHRLGSKNADGK---LSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVTY 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                             14.0%; Score 57; DB 10; Length 506; 32.5%; Pred. No. 20;
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           26; Indels
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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           Mismatches
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CURRENT FILING DATE: 2001-03-21
PRICH APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
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        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-815-242-11757
                                                                                                                                                                       84 -- EALENGISMVHQELNLVL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 --EALENGISMVHQELNLVL 101
                                                                                                                                  62 AGELLLQG---VHDDVDIVL 78
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Yamamoto, Robert T
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Zyskind, Judith W.
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Trawick, John D.
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           Conservative
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      26;
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        APPLICANT: Kyle MacBeth
TITLE OF INVERTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
FILE REFERENCE: 35800/228865
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT APPLICATION NUMBER: US/09/971,791
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 333
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                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                    Length 323;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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Pred. No. 20;
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CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-33
PRIOR PELLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PELLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
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Laura A. Rudolph-Owen
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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32.5%;
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Zyskind, Judith W.
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Best Local Similarity 32.6%
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                           ORGANISM: Xenopus laevis
US-09-971-791-6
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LENGTH: 506
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RESULT 2
US-09-971-791-6
Sequence 6, Application US/09971791
Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
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Sequence 6, Appli
Sequence 1045, Ap
Sequence 11757, A
Sequence 10270, A
Sequence 10270, A
Sequence 10247, A
Sequence 10047, A
Sequence 10, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
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2, Appli
16, Appl
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                                                                                      January 17, 2003, 02:06:44 ; Search time 71 Seconds (without alignments) 22.678 Million cell updates/sec
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1 MNVEHEVNLLVEETHRLGSK.....AGELLLQGVHDDVDIVLLQD
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/NEO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                              120991 seqs, 19878514 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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53.5
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No.
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Sequence 60, Appl Sequence 46512, A Sequence 16, Appl Sequence 2, Appl 1 Sequence 22, Appl 1 Sequence 1559, App Sequence 157, App Sequence 1253, App Sequence 12623, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 5598, Appl Sequence 5383, Appl Sequence 5598, Appl Sequence 5184, Appl Sequence 22, Appl Sequence 224, Appl Sequence 225, Appl Sequence 225, Appl Sequence 225, Appl Sequence 226, Appl	bodies	Length 142; Indels 0; Gaps 0; ALVGTLKAAKRKIVT 60                            ALVGTLKAAKRKIVT 121
US-09-919-497-60 US-09-78-62-16512 US-09-779-307-16 US-09-779-307-16 US-09-738-626-3609 US-09-738-626-698 US-09-712-363-157 US-09-815-242-12623 US-09-815-242-12623 US-09-815-242-12623 US-09-815-242-1624 US-09-815-242-1624 US-09-815-242-1624 US-10-651-909-22 US-09-815-242-1502 US-09-815-242-12502 US-09-815-242-5383 US-09-815-242-5383 US-09-815-242-5383 US-09-816-242-12502 US-09-816-242-12502 US-09-816-242-12503 US-09-816-224 US-09-771-161A-226 US-09-771-161A-226 US-09-815-242-12503 US-09-771-161A-226 US-09-816-226	LIGNMENTS 300 Proteins and Ant 925,300 /05988	tch al Similarity 93.8%; Pred. No. 4.1e-42; 76; Conservative 4; Mismatches 1; Indels 0; G MNVPHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLEALVGTLKAAKRRIVY H
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\$22.55 \$22.55 \$22.55 \$22.55 \$22.55 \$22.55 \$23.55 \$2	ULT 1  09-925-300-1485  iequence 1485, Application l'atent No. US20020151681A1  APPLICANT: Craig Rosen, APPLICANT: Steve Ruben FILLE REFERENCE: PA010  CURRENT ILING DATE: 2001  CURRENT APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-03 NUMBER: PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 1999-03 NUMBER: PRIOR PRIOR FILING DATE: 1999-03 NUMBER: PRIOR PR	Match Local Sin es 76; 1 MNVEHI             61 YAGELI   22 YPGELI
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